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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 43.0833 Seconds  
(without alignments)  
391.341 Million cell updates/sec

Title: US-10-032-376A-8  
Perfect score: 258  
Sequence: 1 LQXLSLPETGELDSATLKA.....VPDLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP97130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	8	ADQ17091 Human mat
4	258	100.0	47	8	ABP69247 Human pol
5	150	58.1	54	5	ABG31461 Peptidase
6	141	54.7	54	6	ABP97127 Human mat
7	141	54.7	54	6	ABG76313 Human mat
8	141	54.7	54	8	ADQ17088 Human mat
9	141	54.7	460	1	AAP93629 Sequence
10	141	54.7	477	2	AAY21993 Human mat
11	141	54.7	477	2	AAY21994 Human mat
12	141	54.7	477	4	ABG84608 Amino aci
13	141	54.7	477	4	AAE10420 Human mat
14	141	54.7	477	4	AAO20482 Prostrone
15	141	54.7	477	5	ABO4752 Human MMP
16	141	54.7	477	6	ABP72353 Matrix me
17	141	54.7	477	6	ABU03473 Angiogene
18	141	54.7	477	6	ABR58544 Human can
19	141	54.7	477	6	ABR32114 Human cer
20	141	54.7	477	6	ABP54461 Matrix me
21	141	54.7	477	7	ADG3273 Human Pro
22	141	54.7	477	7	ADD46343 Human Pro
23	141	54.7	477	7	ADG16014 G-coupled
24	141	54.7	477	7	ADN38704 Cancer/an
25	141	54.7	477	8	ADH42533 Novel hum

26	141	54.7	477	8	ADH42533 Novel hum
27	141	54.7	477	8	ADH42537 Novel hum
28	141	54.7	477	8	ADL93953 Human G-c
29	141	54.7	477	8	ADN07699 Human mat
30	141	54.7	482	8	ADH42531 Novel hum
31	138	53.5	170	1	AAP81873 Partial s
32	135	52.3	173	7	ADE16018 G-coupled
33	135	52.3	173	8	ADL93957 Human G-c
34	135	52.3	477	7	ADG16016 G-coupled
35	135	52.3	477	8	ADH42529 Novel hum
36	135	52.3	477	8	ADH42539 Novel hum
37	135	52.3	477	8	ADL93955 Human G-c
38	134	51.9	463	1	AAP93630 Sequence
39	134	51.9	475	7	ADD46341 Rat Prote
40	134	51.9	475	7	ADE63271 Rat Prote
41	133	51.6	55	6	ABP97128 Human mat
42	133	51.6	55	6	ABG76314 Human mat
43	133	51.6	55	8	ADQ17089 Human mat
44	133	51.6	475	5	ABJ05574 Breast ca
45	133	51.6	475	6	ABU56595 Lung canc

ALIGNMENTS

RESULT 1  
ABP97130  
ID ABP97130 standard; peptide; 47 AA.

XX AC ABP97130;

XX 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
XX KW matrix metalloproteinase inhibitor; antitumor; angiogenic; cardiac;  
XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
XX KW vulnery; cerebroprotective; antidiabetic; ophthalmological; tumour;  
XX KW dermatological; metastatic; non-metastatic; vascularised; heart disease;  
XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
XX KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX WC2003018748-A2.

XX 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quick S. Weart IF.

XX DR WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix

XX metalloproteinase, useful for decreasing the expression of vascular

XX endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX The present invention describes an anti-angiogenic composition (I) for

XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)

XX comprises an effective amount of a peptide inhibitor of matrix

XX metalloproteinase (MMP), where the peptide can inhibit the expression of

XX VEGF. (I) has cytostatic, vulnery cardiac, cerebroprotective,

XX antidiabetic, ophthalmological and dermatological activities. (I) can be

1757 RAL (1329 5.71)

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (1) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47  
 DB 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47

RESULT 2  
 ABG76316  
 ID ABG76316 standard; protein; 47 AA.

XX AC ABG76316;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX KW Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;  
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnery.

XX OS Homo sapiens.

XX PN W0203016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX DR WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix  
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for  
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX PS Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases  
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have  
 CC peptide sequences related to the cleavage regions of the proenzyme forms  
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular  
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin  
 CC development, treating wounds, preventing scarring, improving skin tone,  
 CC reducing wrinkling and for stimulating the development of smooth, healthy  
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing  
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47  
 DB 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47

RESULT 3  
 ADQ17091  
 ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX DE Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX KW Fibronectin; healthy skin; wrinkle; wound; vulnery; dermatological;  
 KW human; matrix metalloproteinase; MMP.

XX OS Homo sapiens.

XX PN US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIR/) QUIRK S.

XX PI Malik S, Quirk S;

XX DR WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds  
 PT comprises peptide having sequence related to matrix metalloproteinase  
 PT proenzyme.

XX Example 1; SEQ ID NO 8; 60pp; English.

XX The present invention provides peptides and compositions containing such  
 CC peptides that are useful as agents to maintain healthy skin and to  
 CC promote the condition of the skin. The invention is useful for increasing  
 CC the amount of fibronectin in tissue. The invention is also useful for  
 CC encouraging the maintenance and development of healthy skin, preventing  
 CC and treating wrinkles and for treating wounds. The invention acts as  
 CC vulnery and dermatological agents. The present sequence is human matrix  
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in  
 CC the exemplification of the invention.

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47  
 DB 1 LQKLSLPETGELDSATLKAMRTRCGVPLGRFQTFEGDLKWHHN 47

RESULT 4

ABP63247  
 ID ABP63247 standard; protein; 432 AA.

XX AC ABP63247;

XX DT 20-JAN-2003 (first entry)

DE Human polypeptide SEQ ID NO 1294.  
 XX  
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270539-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 XX 05-MAR-2002; 2002WO-US0005095.  
 XX  
 XX 05-MAR-2001; 2001US-00799451.  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Dmanac RT;  
 XX  
 XX WPI: 2002-759812/82.  
 DR N-PSDB; ABZ11464.  
 XX  
 XX New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative,  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
 PT or coagulation disorders.  
 XX  
 XX  
 PS Claim 9; SEQ ID NO 1294; 1012pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-  
 CC ABZ12066) or their mature protein coding portion, active domain coding  
 CC protein or complementary sequences. The polynucleotides are useful for  
 CC identifying expressed genes or for physical mapping of human genome. The  
 CC encoded polypeptides (ABZ68902-ABZ69849) are useful as molecular weight  
 CC markers, as a food supplement, for generating antibodies, in medical  
 CC imaging, screening and diagnostic assays and for treating cell-  
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
 CC diabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver  
 CC platelet or coagulation disorders, myeloid or lymphoid disorders,  
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
 CC arthritis, etc. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 432 AA;  
 Query Match 100.0%; Score 258; DB 5; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47  
 DB 74 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 120  
 RESULT 5  
 ABG31461  
 ID ABG31461 standard; protein; 171 AA.  
 XX  
 XX ABG31461;  
 AC  
 XX 29-NOV-2002 (first entry)  
 DT  
 XX

DE Peptidase M10 domain characteristic of metalloproteinases.  
 XX  
 KW Matrix metalloproteinase; MMP 46798; cell proliferation disorder;  
 KW cell differentiation disorder; carcinoma; sarcoma; leukaemia;  
 KW breast cancer; lung cancer; neurological disorder; schizophrenia;  
 KW ischaemia; infarction; Parkinson's disease; Huntington's disease;  
 KW inflammatory disorder; Crohn's disease; immune disorder; arthritis;  
 KW diabetes mellitus; cardiovascular disorder; restenosis; tachycardia;  
 KW rheumatic heart disease; motility disorder; developmental disorder;  
 KW lung disorder; chronic bronchitis; pulmonary congestion; oedema;  
 KW blood disorder; blood clotting disorder; cytostatic; immunomodulator;  
 KW anti-inflammatory; cardiant; antiparkinsonian; nootropic; thrombolytic;  
 KW neuroprotective; antidiabetic; antirheumatic; antiarthritic; vasotropic;  
 KW peptidase M10 domain.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200266670-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-US001546.  
 PF  
 XX 16-JAN-2001; 2001US-0262252P.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Curtis RAJ, Lora JM;  
 PI  
 XX WPI: 2002-674955/72.  
 DR  
 XX New human matrix metalloproteinase nucleic acid and polypeptide  
 PT molecules, designated 46798, useful for diagnosing, preventing or  
 PT treating cancers, ischemia, Parkinson's disease heart disease or edema.  
 XX  
 XX Disclosure; Page 108; 117pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human matrix  
 CC metalloproteinases (MMP), designated 46798, and the polynucleotide  
 CC sequences encoding them. The MMP 46798 polypeptide and polynucleotide  
 CC sequences are useful for diagnosing, preventing, alleviating or treating  
 CC metalloproteinase-associated disorders such as cell proliferation and/or  
 CC differentiation disorders (e.g. carcinoma, sarcoma, leukaemia, breast  
 CC cancer, or lung cancer), neurological disorders (e.g. schizophrenia,  
 CC ischaemia, infarction, Parkinson's disease or Huntington's disease),  
 CC inflammatory disorders (e.g. Crohn's disease), immune disorders (e.g.  
 CC diabetes mellitus or arthritis), cardiovascular disorders (e.g.  
 CC restenosis, tachycardia or rheumatic heart disease), motility disorders,  
 CC developmental disorders, lung disorders (e.g. chronic bronchitis,  
 CC pulmonary congestion or oedema), and blood/blood clotting disorders. The  
 CC present sequence represents a peptidase M10 domain which is  
 CC characteristic of extracellular MMPs  
 XX  
 SQ Sequence 171 AA;  
 Query Match 58.1%; Score 150; DB 5; Length 171;  
 Best Local Similarity 57.4%; Pred. No. 5.1e-13;  
 Matches 27; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 LQKQLSLPTGELDSATLKAMRTPCGVPDLGRFQTFEGDLKWHHN 47  
 DB 32 MKRFEGLPVTKLDSNTLEVNKKPRCGVPDLGRFQTFEGPKWKN 78  
 RESULT 6  
 ABP97127  
 ID ABP97127 standard; peptide; 54 AA.  
 XX  
 XX ABP97127;  
 AC  
 XX 24-JUN-2003 (first entry)  
 DT  
 XX Human matrix metalloproteinase 3 cleavage region peptide SEQ ID NO:5.  
 DE







## RESULT 11

AA21994  
ID AAY21994 standard; protein; 477 AA.

XX AA21994;  
XX  
DT 13-SEP-1999 (first entry)  
XX  
DE Human matrix metalloprotease-3 (MMP-3).  
XX  
XX Matrix metalloprotease-3; MMP-3; modified; human; therapeutic.  
XX

OS Homo sapiens.

PN JP11169176-A.

XX 29-JUN-1999.

XX 15-DEC-1997; 97JP-00345008.

XX 15-DEC-1997; 97JP-00345008.

XX (YAMA ) YAMANOUCHI PHARM CO LTD.

XX WPI; 1999-422616/36.

DR N-PSDB; AAX89009.

XX A modified matrix metalloprotease-3 - used in the production of

PT therapeutics.

XX Claim 1; Page 10-11; 17pp; Japanese.

XX The invention describes a modified matrix metalloprotease-3 (MMP-3) that

CC has an amino acid (aa) sequence (AAY21994) in which the (i) the aa

CC residue at position 172 (Xaa) from the N terminal is modified by -Ile- or

CC -Tyr-; (ii) the aa residue at position 239 (Xaa) is modified by -Val- or

CC -Leu-; (iii) the aa residues at position from 241 to 243 (-Xaa-Xaa-Xaa-)

CC are modified by continuous -His-Ser-Leu- or -Asn-Ala-Phe- and have an

CC active domain or an active domain in which the aa residues of the

CC sequence are replaced, deleted or inserted at at least aa residues from

CC 100 to 274 from the N terminal and being stable, provided that a case is

CC not selected in which the aa residue: 172 (Xaa) is -Tyr, the 239 (Xaa) is

CC -Leu- and 241 to 243 (-Xaa-Xaa-Xaa-) are -His-Ser-Leu-. A host cell

CC transformed by a vector comprising the DNA encoding the MMP-3 can be used

CC for the recombinant preparation of MMP-3. The MMP-3 or its fragment have

CC high stability and can be used in the production of therapeutics. The

CC present sequence represents a human MMP-3 of the invention

XX

SQ Sequence 477 AA;

Query Match 54.7%; Score 141; DB 2; Length 477;

Best Local Similarity 62.8%; Pred. No. 3.5e-11;

Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPCGVPDLGRTFQTEGDLKW 43

DB 67 MQKFLGLEVTGKLDSDTLEVMRPRCGVPDVGHRTFPGIPKW 109

RESULT 12

AA284608

ID AAB84608 standard; protein; 477 AA.

XX AA284608;

XX 05-SEP-2001 (first entry)

XX Amino acid sequence of matrix metalloproteinase-3 stromelysin 1.

XX Growth factor; protein inhibitor; protease; damaged tissue;

XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;

XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;

XX

KW

KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;

KW transforming growth factor-beta; TGF-beta; matrix metalloprotease; MMP;

KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;

KW vascular endothelial growth factor; urokinase plasminogen activator;

KW dermal ulcer; wound.

XX

OS Homo sapiens.

XX WO200149309-A2.

PN 12-JUL-2001.

XX 21-DEC-2000; 2000WO-IB001935.

XX 29-DEC-1999; 99GB-00030768.

XX (PFIZ ) PFIZER LTD.

PA (PFIZ ) PFIZER INC.

XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;

XX WPI; 2001-418351/44.

DR N-PSDB; AAH28223.

XX Composition for the treatment of damaged tissue i.e. chronic wounds and

PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth

PT factor.

XX Disclosure; Page 554; 572pp; English.

XX The specification describes a pharmaceutical composition, comprising a

CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent

CC inhibits the action of at least one specific adverse protein, i.e. a

CC protease, that is upregulated in a damaged tissue such as a wound

CC environment. Growth factors which are included in the composition of the

CC invention are platelet-derived growth factor (PDGF), fibroblast growth

CC factor (FGF), connective tissue derived growth factor (CTGF),

CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta

CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),

CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),

CC and chrysalin. Inhibitors which are included in the composition of the

CC invention include inhibitors of urokinase-type plasminogen activator

CC (uPA) and matrix metalloprotease (MMP). The composition is useful for

CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.

CC The present sequence represents a human MMP-3, and is used to produce the

CC composition of the invention

XX

SQ Sequence 477 AA;

Query Match 54.7%; Score 141; DB 4; Length 477;

Best Local Similarity 62.8%; Pred. No. 3.5e-11;

Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 LKQLSLPETGELDSATLKAMRTPCGVPDLGRTFQTEGDLKW 43

DB 67 MQKFLGLEVTGKLDSDTLEVMRPRCGVPDVGHRTFPGIPKW 109

RESULT 13

AAE10420

ID AAE10420 standard; protein; 477 AA.

XX AAE10420;

XX 10-DEC-2001 (first entry)

XX Human matrix metalloproteinase-3 (MMP-3) protein.

XX Human; matrix metalloproteinase; MMP-3; hair growth; antisense therapy;

XX endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.

XX Homo sapiens.

XX

```
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= Signal_peptide
FT Protein 18..477
FT /label= Mature_MMP_3_protein
FT Domain 90..96
FT /label= Cysteine_switch_domain
FT Domain 161..185
FT /note= "Zinc and calcium binding domain"
XX
XX WO200166766-A2.
XX
XX 13-SEP-2001.
XX
XX 06-MAR-2001; 2001WO-US007167.
XX
XX 06-MAR-2000; 2000US-0187196P.
XX
XX (DARW-) DARWIN MOLECULAR CORP.
XX (SCHA/) SCHATZMAN R.
XX
XX Fajardo M, Wang K, Smith R, Moss P;
XX
XX WPI; 2001-582276/65.
XX
XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
XX proteins encoded by them whose inhibition is useful for modulation of
XX hair growth in mammals.
XX
XX Example 2; Fig 3; 119pp; English.
XX
XX The present sequence is human matrix metalloproteinase (MMP)-3 protein
XX used in the exemplification of the invention. MMP-25 DNA is located on
XX chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX dependent endopeptidases that function extracellularly to degrade
XX proteins typically found in the extracellular matrix. MMP-25 is expressed
XX in skin cells of mammals, particularly in breast cells and hair
XX follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX sample and identifying a sequence that hybridises in the nucleic acid
XX sample. The identification step involves performing polymerase chain
XX reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX to modulate hair growth and breast cancer in a mammal
XX
XX Sequence 477 AA;
XX
XX Query Match 54.7%; Score 141; DB 4; Length 477;
XX Best Local Similarity 62.8%; Pred. No. 3.5e-11;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSLPETGELDSATLKAMRTRPGVDPDLGRFQTFEGDLKW 43
XX Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVPDVGHFRTFPGIPKW 109
XX
XX RESULT 14
XX AAO20482
XX ID AAO20482 standard; protein; 477 AA.
XX
XX AC AAO20482;
XX
XX DT 27-JUN-2002 (first entry)
XX
XX DE Prostromelysin protein.
XX
XX Osteopathic; dermatological; vulnery; catalytic domain; propeptide;
XX human; stromelysin; matrix metalloproteinase; SCD; scar tissue formation;
XX herniated vertebral disc; dermal ulcer; joint disease; protein therapy;
XX prostromelysin.
XX
XX Homo sapiens.
XX
XX OS
```

```
FH Key Location/Qualifiers
FT Peptide 1..17
FT /note= "Signal peptide"
FT Peptide 18..99
FT /note= "Propeptide"
FT Protein 100..273
FT /note= "Mature stromelysin catalytic domain protein"
XX
XX US6284513-B1.
XX
XX 04-SEP-2001.
XX
XX 27-JUL-1994; 94US-00281313.
XX
XX 03-FEB-1993; 93US-00012705.
XX (WARN ) WARNER LAMBERT CO.
XX
XX Ye Q, Johnson LL, Hupe DJ, Baragi V;
XX
XX WPI; 2001-615435/71.
XX
XX One step in vivo process for producing stromelysin catalytic domain,
XX which is useful in treating e.g. dermal ulcers or herniated vertebral
XX discs, by culturing transformed Escherichia coli having a gene encoding
XX the catalytic domain.
XX
XX Disclosure; Fig 1; 16pp; English.
XX
XX The invention relates to a one-step in vivo process for producing a
XX catalytic domain, without propeptide, of human stromelysin, comprising
XX culturing transformed Escherichia coli host cells comprising a DNA
XX sequence encoding the catalytic domain. For producing the catalytic
XX domain, without propeptide, of a matrix metalloproteinase, particularly
XX of the stromelysin catalytic domain. The stromelysin catalytic domain
XX (SCD) protein is useful in treating herniated vertebral discs, dermal
XX ulcers or joint diseases, or modifying scar tissue formation by means of
XX protein therapy. This sequence represents the prostromelysin protein of
XX the invention
XX
XX Sequence 477 AA;
XX
XX Query Match 54.7%; Score 141; DB 4; Length 477;
XX Best Local Similarity 62.8%; Pred. No. 3.5e-11;
XX Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 1 LQKQLSLPETGELDSATLKAMRTRPGVDPDLGRFQTFEGDLKW 43
XX Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVPDVGHFRTFPGIPKW 109
XX
XX RESULT 15
XX ABB04752
XX ID ABB04752 standard; protein; 477 AA.
XX
XX AC ABB04752;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human MMP3 protein SEQ ID NO:3.
XX
XX Human; matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP;
XX haplotype; polymorphism; polymorphic; single nucleotide polymorphism;
XX probe; primer; detection; genotyping; vulnery; cytostatic; cancer;
XX antiarteriosclerotic; gene therapy; coronary atherosclerosis;
XX wound healing.
XX
XX Homo sapiens.
XX
XX WO200179238-A2.
XX
XX 25-OCT-2001.
XX
```

PF 17-APR-2001; 2001WO-US012452.  
XX  
PR 17-APR-2000; 2000US-0197911P.  
PR 13-JUL-2000; 2000US-0218092P.  
XX  
XX PA (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;  
XX  
XX NPI; 2002-075067/10.  
DR N-PSDB; ABL01224.  
XX  
XX Genotyping human matrix metalloproteinase 3 gene of an individual for  
PT determining the haplotype of the individual, comprises determining the  
PT identity of a nucleotide pair at specific polymorphic sites for two  
PT copies of the gene.  
XX  
XX Claim 27; Fig 3; 83pp; English.  
XX  
XX The present invention describes a method for genotyping a human matrix  
CC metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary,  
CC cytostatic and antiarteriosclerotic activity, and can be used in gene  
CC therapy. The method can be used for improving the efficacy and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with MMP3 activity, e.g., wound healing,  
CC cancer and coronary atherosclerosis; to validate MMP3 as a candidate  
CC agent for treating a specific condition or disease predicted to be  
CC associated with MMP3 activity; and in the design of clinical trials of  
CC candidate drugs for treating a specific condition or disease predicted to  
CC be associated with MMP3 activity. Polymorphic variants of a reference  
CC sequence for MMP3 (see ABL01223) are useful in studying the expression  
CC and function of MMP3, and in expressing MMP3 protein for use in screening  
CC for candidate drugs to treat diseases related to MMP3 activity. The human  
CC MMP3 gene is located on chromosome 11q22.3. ABL01225 to ABL01246 and  
CC ABL01247 to ABL01290 represent allele-specific oligonucleotide (ASO)  
CC probes and primers used in the detection of polymorphisms in the human  
CC MMP3 gene. ABL01291 to ABL01334 represent preferred primers used in the  
CC detection of polymorphisms in the human MMP3 gene. The present sequence  
CC represents the human MMP3 protein, as given in the present invention  
XX  
XX SQ Sequence 477 AA;  
  
Query Match 54.7%; Score 141; DB 5; Length 477;  
Best Local Similarity 62.8%; Pred. No. 3.5e-11;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 LQQLSLPETGELDSATLKAMRTPRCVDPDLGRFQTFEGDLKW 43  
Db 67 MQKFLGLEVTGKLDSDTLEVMKRCVDPDVGHFRFTFGIPKW 109  
  
Search completed: November 15, 2004, 14:04:07  
Job time : 45.0833 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.638 Seconds  
(without alignments)  
246.324 Million cell updates/sec

Title: US-10-032-376A-8  
Perfect score: 258  
Sequence: 1 LQKLSLPTGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	141	54.7	477	3	US-08-704-711A-20
2	141	54.7	477	3	US-08-448-489-15
3	141	54.7	477	3	US-08-281-313-1
4	141	54.7	477	3	US-09-521-220-20
5	141	54.7	477	3	US-09-391-104-21
6	133	51.6	476	3	US-08-704-711A-21
7	133	51.6	476	3	US-08-448-489-14
8	133	51.6	476	3	US-09-521-220-21
9	133	51.6	476	3	US-09-391-104-22
10	117	45.3	471	3	US-09-391-104-25
11	115	44.6	136	4	US-09-513-999C-4639
12	114	44.2	631	3	US-08-448-489-17
13	114	44.2	660	3	US-08-704-711A-18
14	114	44.2	660	3	US-09-521-220-18
15	114	44.2	660	3	US-09-391-104-19
16	114	44.2	660	4	US-09-517-254-89
17	113	43.8	470	3	US-08-068-392-2
18	113	43.8	470	3	US-08-396-988-2
19	113	43.8	470	3	US-09-391-104-26
20	110	42.6	469	3	US-08-704-711A-16
21	110	42.6	469	3	US-08-448-489-12
22	110	42.6	469	3	US-09-521-220-16
23	110	42.6	469	3	US-09-391-104-23
24	109	42.2	513	4	US-10-140-002-192
25	109	42.2	513	4	US-09-862-631-4
26	108	41.9	471	4	US-08-994-689C-1
27	107	41.5	135	4	US-09-513-999C-4163

## ALIGNMENTS

## RESULT 1

US-08-704-711A-20  
; Sequence 20, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Hardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-20

28 106 41.1 267 3 US-08-448-489-18  
29 106 41.1 267 3 US-09-391-104-27  
30 106 41.1 271 3 US-08-896-062-2  
31 105 40.7 264 3 US-09-009-156-6  
32 105 40.7 264 3 US-09-372-154-6  
33 101 39.1 471 4 US-08-994-689C-21  
34 100.5 39.0 582 3 US-08-704-711A-2  
35 100.5 39.0 582 3 US-08-448-489-1  
36 100.5 39.0 582 3 US-09-211-704A-9  
37 100.5 39.0 582 3 US-09-521-220-2  
38 100.5 39.0 582 3 US-09-391-104-28  
39 100.5 39.0 582 4 US-09-919-497-84  
40 100 38.8 444 1 US-09-178-002-2  
41 100 38.8 466 3 US-08-704-711A-17  
42 100 38.8 466 3 US-09-521-220-17  
43 100 38.8 467 1 US-09-178-002-4  
44 100 38.8 467 3 US-09-391-104-24  
45 100 38.8 468 3 US-08-448-489-13

Sequence 18, Appl  
Sequence 27, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 21, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 9, Appl  
Sequence 2, Appl  
Sequence 28, Appl  
Sequence 84, Appl  
Sequence 2, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 4, Appl  
Sequence 24, Appl  
Sequence 13, Appl



Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

**Qy**

1 L Q K Q L S P E T G E L D S A I L K A M R T P R C G V P D L G R F Q T F E G D L K W    43  
: : : : : : : : : : : : : : : : :

**D6**

67 M Q K F L G L E V T G K L D S D T L E W N R K P R C G V P D V G H F R T F P G I P K W    109

## RESULT 4

US-09-521-220-20  
; Sequence 20, Application US/09521220  
; Patent No. 6399348  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; HINZMANN, Bernd

TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
METALLOPROTEASES, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

```

; *****
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/521,220  
FILING DATE: 08-Mar-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
21-OCT-1994  
17-MAR-1994

APPLICATION NUMBER: 08/704,711  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANAOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399

TELEX: 904136  
INFORMATION FOR SEQ ID NO: 20:

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SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID
US-09-521-320-20

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Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27; Conservative 5; Mismatches 11; Indels

Qy 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLPQTFEGDLKW 43  
: | | | | | : | | | | | : | | | | |  
Db 67 MOKFGLVETGKLDSDTLFVMRKPRCGVDPDVGHFTFPFGIPKW 109

DEBIT

RESULT 5  
US-09-391-104-21  
: Sequence 21, Application US/09391104

; Patent No. 6399371  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Abbott Laboratories  
 ;  
 ; APPLICANT: Falduto, Michael T.  
 ;  
 ; APPLICANT: Magnuson, Scott R.  
 ;  
 ; APPLICANT: Morisan, Douglas W.  
 ;  
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
 ;  
 ; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
 ;  
 ; TITLE OF INVENTION: OF USING SAME

FILE REFERENCE: 6073.US.P1  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07

; CURRENT FILING DATE: 1999-09-07  
 ; PRIOR APPLICATION NUMBER: US 08/814,394  
 ; PRIOR FILING DATE: 1997-03-11

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; TRACKER RUNNING SINCE: 1997-09-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21

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; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-21

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Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27: Conservative 5; Mismatches 11; Indels

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QY      1 LQQLSLPETGELDSATLKAMRTPCGVPLGRFQTFEGDLKW 43
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DB     67 MKEFGLVETGKLDSDTLVAMRKPCGVPLVGHFRTFPGIPKW 105
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## RESULT 6

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US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

```

STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0  
version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995

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PRIOR APPLICATION DATA: DE 443838.1  
APPLICATION NUMBER: DE 443838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA: DE 443838.1  
APPLICATION NUMBER: DE 443838.1  
FILING DATE: 21-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399

```
;
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-21

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDITLVMRKPRCGVDPDVGHFSFPGMPKW 108

RESULT 7
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: SS-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
; US-08-448-489-14

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDITLVMRKPRCGVDPDVGHFSFPGMPKW 108

RESULT 8
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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;
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4496663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDITLVMRKPRCGVDPDVGHFSFPGMPKW 108

RESULT 9
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-22

Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43
Db 66 MQKFLGLEVTGKLDTDITLVMRKPRCGVDPDVGHFSFPGMPKW 108

RESULT 10
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US-09-391-104-25
; Sequence 25, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.F1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-25

Query Match 45.3%; Score 117; DB 3; Length 471;
Best Local Similarity 46.8%; Pred. No. 8.5e-09;
Matches 22; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAVRTPRCGVPDGLGRFQTPEGDLKWHHN 47
Db 71 MQSFFGLEVTGKLDNDTLDVYMKPRCGVPDVGSEYVFPRTLKWSQXN 117

RESULT 11
US-09-513-999C-4639
; Sequence 4639, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4639
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -29...-1
; OTHER INFORMATION: score 11.4
; OTHER INFORMATION: seq LCLLGCLLSHAAA/AP
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 16
; OTHER INFORMATION: Xaa=Lys or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 17
; OTHER INFORMATION: Xaa=Asp or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 19
; OTHER INFORMATION: Xaa=Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE

US-09-391-104-25
; LOCATION: 22
; OTHER INFORMATION: Xaa=Leu or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 26
; OTHER INFORMATION: Xaa=Lys or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa=Ile or Asn or Ser or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 33
; OTHER INFORMATION: Xaa=Lys or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 34
; OTHER INFORMATION: Xaa=Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 66
; OTHER INFORMATION: Xaa=Asp or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 67
; OTHER INFORMATION: Xaa=Ala or Pro or Ser or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 75
; OTHER INFORMATION: Xaa=Lys or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 80
; OTHER INFORMATION: Xaa=Lys or Asn or Arg or Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 88
; OTHER INFORMATION: Xaa=Ala or Cys or Asp or Phe or Gly or His or Ile or Leu or Asn
; OTHER INFORMATION: Tyr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 104
; OTHER INFORMATION: Xaa=Ala or Pro
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US-09-513-999C-4639

Query Match 44.6%; Score 115; DB 4; Length 136;
Best Local Similarity 46.5%; Pred. No. 3.4e-09;
Matches 20; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAVRTPRCGVPDGLGRFQTPEGDLKW 43
Db 77 MQKFFGLPQTGDLDDQNTIXXMKPRCGXPVDVAXYFFPRXXKW 119

RESULT 12
US-08-448-489-17
; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
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; FILE REFERENCE: 6073-US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19
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Best Local Similarity 46.5%; Pred. No. 3.7e-08;
Matches 20; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Qy      1 LQQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43
       :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      77 MQKFFGLPQTGDLDDQNTIETMRKPCRCNPDVANYNFFPKPKW 119
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Search completed: November 15, 2004, 14:08:07
Job time : 13.6538 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 121.718 Seconds  
(without alignments)  
136.623 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LOKLSLPETGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	47	14 US-10-219-329-8	Sequence 8, Appli
2	258	100.0	47	14 US-10-153-185-8	Sequence 8, Appli
3	258	100.0	47	14 US-10-219-561-8	Sequence 8, Appli
4	258	100.0	47	16 US-10-032-376A-8	Sequence 8, Appli
5	258	100.0	47	16 US-10-335-207-8	Sequence 8, Appli
6	150	58.1	171	14 US-10-050-216B-4	Sequence 4, Appli
7	141	54.7	54	14 US-10-219-329-5	Sequence 5, Appli
8	141	54.7	54	14 US-10-153-185-5	Sequence 5, Appli
9	141	54.7	54	14 US-10-219-561-5	Sequence 5, Appli
10	141	54.7	54	16 US-10-032-376A-5	Sequence 5, Appli
11	141	54.7	54	16 US-10-335-207-5	Sequence 5, Appli
12	141	54.7	267	14 US-10-133-797-73	Sequence 73, Appli
13	141	54.7	477	9 US-09-391-104-21	Sequence 21, Appli

141	54.7	477	9	US-09-801-196-24	Sequence 24, Appli
141	54.7	477	14	US-10-171-311-137	Sequence 137, Appli
141	54.7	477	14	US-10-301-822-127	Sequence 127, Appli
141	54.7	477	14	US-10-131-985-27	Sequence 27, Appli
141	54.7	477	14	US-10-295-027-22	Sequence 22, Appli
141	54.7	477	15	US-10-115-479-44	Sequence 44, Appli
141	54.7	477	15	US-10-211-462-36	Sequence 36, Appli
141	54.7	477	15	US-10-447-315-5	Sequence 5, Appli
141	54.7	477	15	US-10-115-479-48	Sequence 48, Appli
141	54.7	477	15	US-10-115-479-46	Sequence 46, Appli
141	54.7	477	15	US-10-219-329-6	Sequence 6, Appli
141	54.7	477	15	US-10-153-185-8	Sequence 6, Appli
141	54.7	477	15	US-10-219-561-6	Sequence 6, Appli
141	54.7	477	15	US-10-032-376A-6	Sequence 6, Appli
141	54.7	477	15	US-10-335-207-6	Sequence 6, Appli
141	54.7	477	15	US-10-295-027-8	Sequence 8, Appli
141	54.7	477	15	US-10-058-370A-78	Sequence 78, Appli
141	54.7	477	9	US-09-391-104-22	Sequence 22, Appli
141	54.7	477	9	US-09-801-196-25	Sequence 25, Appli
141	54.7	477	14	US-10-021-860-72	Sequence 72, Appli
141	54.7	477	14	US-10-131-985-35	Sequence 35, Appli
141	54.7	477	15	US-10-211-462-10	Sequence 10, Appli
141	54.7	477	15	US-10-188-832-4	Sequence 4, Appli
141	54.7	477	9	US-09-920-455-260	Sequence 260, Appli
141	54.7	477	9	US-10-219-329-3	Sequence 3, Appli
141	54.7	477	14	US-10-153-185-3	Sequence 3, Appli
141	54.7	477	14	US-10-219-561-3	Sequence 3, Appli
141	54.7	477	15	US-10-032-376A-3	Sequence 3, Appli
141	54.7	477	15	US-10-335-207-3	Sequence 3, Appli
141	54.7	477	14	US-10-409-643-21	Sequence 21, Appli
141	54.7	477	9	US-09-391-104-25	Sequence 25, Appli
141	54.7	477	9	US-09-801-196-21	Sequence 21, Appli

ALIGNMENTS

RESULT 1  
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; Sequence 8, Application US/10219329  
; Publication No. US20030096757A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds  
; FILE REFERENCE: 1443.035W01  
; CURRENT APPLICATION NUMBER: US/10/219,329  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 47  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-329-8

Query Match 100.0%; Score 258; DB 14; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.1e-27;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKLSLPETGELDSATLKAMRTPCGVPDILGRFQTFEGDLKWHHN 47  
DB 1 LOKLSLPETGELDSATLKAMRTPCGVPDILGRFQTFEGDLKWHHN 47

RESULT 2  
US-10-153-185-8  
; Sequence 8, Application US/10153185  
; Publication No. US20030148959A1

Query Match	Best Local Similarity	Score	DB 14;	Length	DB 16;	Length	DB 17;	Length
Query Match	Best Local Similarity	Score	DB 14;	Length	DB 16;	Length	DB 17;	Length
Matches	47; Conservative	0; Mismatches	0; Indels	0; Gaps	0; Indels	0; Gaps	0; Indels	0; Gaps
QY	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
Db	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
RESULT 3	US-10-219-561-8	100.0%;	Score 258;	DB 14;	Length 47;			
Sequence 8, Application US/10219561	Publication No. US20030166567A1	GENERAL INFORMATION:	APPLICANT: Quirk, Stephen	APPLICANT: Villanueva, Julie M.	TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds	FILE REFERENCE: 1443.008US2	CURRENT APPLICATION NUMBER: US 10/219,561	CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376	PRIOR FILING DATE: 2001-12-21	PRIOR APPLICATION NUMBER: US 10/153,185	PRIOR FILING DATE: 2002-05-21	PRIOR APPLICATION NUMBER: US 60/312,726	PRIOR FILING DATE: 2001-08-16	NUMBER OF SEQ ID NOS: 21	SOFTWARE: FastSeq for Windows Version 4.0	SEQ ID NO 8
TYPE: PRT	ORGANISM: Homo sapiens	LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens	LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens	LENGTH: 47
US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8	US-10-219-561-8
Query Match	Best Local Similarity	Score	DB 14;	Length	DB 16;	Length	DB 17;	Length
Matches	47; Conservative	0; Mismatches	0; Indels	0; Gaps	0; Indels	0; Gaps	0; Indels	0; Gaps
QY	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
Db	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
RESULT 4	US-10-032-376A-8	100.0%;	Score 258;	DB 14;	Length 47;			
Sequence 8, Application US/10032376A	Publication No. US20040127420A1	GENERAL INFORMATION:	APPLICANT: Quirk, Steven	APPLICANT: Villanueva, Julie M.	TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing	FILE REFERENCE: 1443.008US1	CURRENT APPLICATION NUMBER: US/10/032,376A	CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/032,376	PRIOR FILING DATE: 2001-12-21	PRIOR APPLICATION NUMBER: US 60/312,726	PRIOR FILING DATE: 2001-08-16	NUMBER OF SEQ ID NOS: 20	SOFTWARE: FastSeq for Windows Version 4.0	SEQ ID NO 8	TYPE: PRT	ORGANISM: Homo sapiens
LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens	LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens	LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens
US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8	US-10-032-376A-8
Query Match	Best Local Similarity	Score	DB 14;	Length	DB 16;	Length	DB 17;	Length
Matches	47; Conservative	0; Mismatches	0; Indels	0; Gaps	0; Indels	0; Gaps	0; Indels	0; Gaps
QY	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
Db	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 14;	Length 47;			
RESULT 5	US-10-335-207-8	100.0%;	Score 258;	DB 16;	Length 47;			
Sequence 8, Application US/10335207	Publication No. US20040127421A1	GENERAL INFORMATION:	APPLICANT: Malik, Sohail	APPLICANT: Quirk, Stephen	TITLE OF INVENTION: Method to Increase Fibronectin	FILE REFERENCE: 1443.047US1	CURRENT APPLICATION NUMBER: US/10/335,207	CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/335,207	PRIOR FILING DATE: 2002-12-30	NUMBER OF SEQ ID NOS: 21	SOFTWARE: FastSeq for Windows Version 4.0	SEQ ID NO 8	LENGTH: 47	TYPE: PRT	ORGANISM: Homo sapiens	US-10-335-207-8
US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8	US-10-335-207-8
Query Match	Best Local Similarity	Score	DB 16;	Length	DB 17;	Length	DB 18;	Length
Matches	47; Conservative	0; Mismatches	0; Indels	0; Gaps	0; Indels	0; Gaps	0; Indels	0; Gaps
QY	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 16;	Length 47;			
Db	1 LOKQLSLPETGELDSATLKA	100.0%;	Score 258;	DB 16;	Length 47;			
RESULT 6	US-10-050-216B-4	100.0%;	Score 258;	DB 14;	Length 47;			
Sequence 4, Application US/10050216B	Publication No. US20030039991A1	GENERAL INFORMATION:	APPLICANT: Curtis, Rory A.J., Lora, Jose M.	APPLICANT: Villanueva, Julie M.	TITLE OF INVENTION: A Human Matrix Metalloprotease and	FILE REFERENCE: MPI2001-014PIRNM	CURRENT APPLICATION NUMBER: US/10/050,216B	CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 60/262,252	PRIOR FILING DATE: 2001-01-16	NUMBER OF SEQ ID NOS: 10	SOFTWARE: FastSeq for Windows Version 4.0	SEQ ID NO 4	LENGTH: 171	TYPE: PRT	ORGANISM: Artificial Sequence	FEATURE:
OTHER INFORMATION: Consensus	US-10-050-216B-4	US-10-050-2						

Qy 1 LQKQSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47  
Db 32 MQKFFGLPVTGKLDSTLEVMKXPRCGVDPDVGERTFPGSPKWSKN 78

RESULT 7  
US-10-219-329-5  
; Sequence 5, Application US/10219329  
; Publication No. US20030096757A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Weart, Ilona f.  
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds  
; FILE REFERENCE: 1443.03SWO1  
; CURRENT APPLICATION NUMBER: US/10/219,329  
; PRIOR FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-329-5

Query Match 54.7%; Score 141; DB 14; Length 54;  
Best Local Similarity 62.8%; Pred. No. 1.4e-11;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKQSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLK 43  
Db 1 MQKFLGLEVTGKLDSTLEVMKXPRCGVDPDVGERTFPGIPK 43

RESULT 8  
US-10-153-185-5  
; Sequence 5, Application US/10153185  
; Publication No. US20030148959A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds  
; FILE REFERENCE: 1443.034US1  
; CURRENT APPLICATION NUMBER: US/10/153,185  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US 10/032,376  
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; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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US-10-219-561-5  
; Sequence 5, Application US/10219561

; Publication No. US20030166567A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; APPLICANT: Villanueva, Julie M.  
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds  
; FILE REFERENCE: 1443.008US2  
; CURRENT APPLICATION NUMBER: US/10/219,561  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 10/153,185  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-561-5

Query Match 54.7%; Score 141; DB 14; Length 54;  
Best Local Similarity 62.8%; Pred. No. 1.4e-11;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKQSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLK 43  
Db 1 MQKFLGLEVTGKLDSTLEVMKXPRCGVDPDVGERTFPGIPK 43

RESULT 10  
US-10-032-376A-5  
; Sequence 5, Application US/10032376A  
; Publication No. US20040127420A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Steven  
; TITLE OF INVENTION: Metalloprotease Inhibitors for Wound Healing  
; FILE REFERENCE: 1443.008US1  
; CURRENT APPLICATION NUMBER: US/10/032,376A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-376A-5

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Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKQSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLK 43  
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RESULT 11  
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; Sequence 5, Application US/10335207  
; Publication No. US20040127421A1  
; GENERAL INFORMATION:  
; APPLICANT: Malik, Sohail  
; APPLICANT: Quirk, Stephen  
; TITLE OF INVENTION: Method to Increase Fibronectin  
; FILE REFERENCE: 1443.047US1  
; CURRENT APPLICATION NUMBER: US/10/335,207  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 54

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-335-207-5

Query Match 54.7%; Score 141; DB 16; Length 54;  
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Db 1 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKW 43

RESULT 12

US-10-133-797-73

; Sequence 73, Application US/10133797

; Publication No. US20030109021A1

; GENERAL INFORMATION:

; APPLICANT: Wu, Shujian

; APPLICANT: Chen, Jian

; APPLICANT: Feder, John

; APPLICANT: Lee, Liana

; APPLICANT: Krystek, Stanley

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL METALLOPROTEASE HIGHLY EXPRESSED IN THE TESTIS, MMP-29

; FILE REFERENCE: D0141NP

; CURRENT APPLICATION NUMBER: US/10/133,797

; PRIOR FILING DATE: 2002-04-26

; PRIOR APPLICATION NUMBER: US 60/286,764

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 73

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-133-797-73

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Best Local Similarity 62.8%; Pred. No. 8.6e-11;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43  
Db 26 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKW 68

RESULT 13

US-09-391-104-21

; Sequence 21, Application US/09391104

; Publication No. US200301817A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Falduto, Michael T.

; APPLICANT: Magnuson, Scott R.

; APPLICANT: Morgan, Douglas W.

; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,

; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

; TITLE OF INVENTION: OF USING SAME

; FILE REFERENCE: 6073.US.P1

; CURRENT APPLICATION NUMBER: US/09/391,104

; CURRENT FILING DATE: 1999-09-07

; PRIOR APPLICATION NUMBER: US 08/814,394

; PRIOR FILING DATE: 1997-03-11

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 477

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-391-104-21

Query Match 54.7%; Score 141; DB 9; Length 477;  
Best Local Similarity 62.8%; Pred. No. 1.7e-10;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43  
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKW 109

RESULT 14

US-09-801-196-24

; Sequence 24, Application US/09801196

; Patent No. US20020037827A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Kai

; APPLICANT: Smith, Ryan

; APPLICANT: Fajardo, Mark

; APPLICANT: Moss, Patrick

; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)

; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS

; FILE REFERENCE: 240083.509

; CURRENT APPLICATION NUMBER: US/09/801,196

; CURRENT FILING DATE: 2001-03-06

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 477

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-801-196-24

Query Match 54.7%; Score 141; DB 9; Length 477;  
Best Local Similarity 62.8%; Pred. No. 1.7e-10;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43  
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKW 109

RESULT 15

US-10-171-311-137

; Sequence 137, Application US/10171311

; Publication No. US20030087270A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Chen, Yan

; APPLICANT: Zhao, Xumei

; APPLICANT: Monahan, John

; APPLICANT: Kamatkar, Shubhangi

; APPLICANT: Glatt, Karen

; APPLICANT: Gannavarapu, Manjula

; APPLICANT: Hoersch, Sebastian

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

; TITLE OF INVENTION: OF CERVICAL CANCER

; FILE REFERENCE: MEI-035

; CURRENT APPLICATION NUMBER: US/10/171,311

; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,155

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/335,936

; PRIOR FILING DATE: 2001-11-14

; NUMBER OF SEQ ID NOS: 238

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 137

; LENGTH: 477

; TYPE: PRT

; ORGANISM: Homo sapiens



Search completed: November 15, 2004, 14:22:34  
Job time : 122.718 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 10.5449 Seconds  
(without alignments)  
428.852 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPFGELDSATLKA.....VPLGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246014

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	141	54.7	477	1 KCHUS1	stromelysin 1 (EC
2	138	53.5	478	1 KCRBS1	stromelysin 1 (EC
3	134	51.9	475	1 KCRTH	stromelysin 1 (EC
4	133	51.6	476	1 JC6505	stromelysin 2 (EC
5	133	51.6	476	1 KCHUS2	stromelysin 2 (EC
6	133	51.6	476	1 KCRS2	stromelysin 1 (EC
7	133	51.6	477	1 KCMSS1	stromelysin 1 (EC
8	121	46.9	472	2 S29243	interstitial colla
9	118	45.7	466	2 A23685	interstitial colla
10	117	45.3	471	2 A53711	collagenase 3 (EC
11	116	45.0	267	2 A57490	matrilysin (EC 3.4
12	114	44.2	660	1 A28153	gelatinase A (EC 3.4
13	113	43.8	470	2 A49499	metalloelastase HM
14	110	42.6	469	1 KCHUI	interstitial colla
15	108	41.9	82	2 JC5743	pro-matrix metallo
16	108	41.9	483	2 JC5743	matrix metalloprot
17	106	41.1	267	1 KCHUM	matrilysin (EC 3.4
18	104.5	40.5	582	2 I84871	matrix metalloprot
19	103	39.9	468	1 KCRBI	interstitial colla
20	100.5	39.0	582	2 I38028	matrix metalloprot
21	100	38.8	467	1 KCHUN	neutrophil collage
22	99	38.4	469	1 KCHUI	interstitial colla
23	98	38.0	469	1 KCB01	interstitial colla
24	97.5	37.8	582	2 I48573	matrix metalloprot
25	96	37.2	521	2 T37252	probable matrix me
26	92	35.7	364	2 E71433	probable metallopr
27	92	35.7	462	2 A42401	macrophage elastas
28	91	35.3	616	2 JC7776	matrix metalloprot
29	88	34.1	305	2 T08936	probable metallopr

30	85.5	33.1	341	2	T51957	metalloproteinase
31	85.5	33.1	342	2	G84885	probable metallopr
32	83.5	32.4	378	2	E96724	hypothetical prote
33	80	31.0	587	2	S12805	envelysin (EC 3.4.
34	79.5	30.8	508	2	JC5082	matrix metalloprot
35	75.5	29.3	384	2	I51267	collagenase (EC 3.
36	75	29.1	377	2	T00643	zinc metalloprotei
37	73	28.3	587	2	S41409	envelysin (EC 3.4.
38	67.5	26.2	478	2	T32825	hypothetical prote
39	60	23.3	136	1	TCRT	calcitonin precurs
40	59	22.9	579	2	T37248	probable matrix me
41	59	22.9	598	2	T32165	hypothetical prote
42	57	22.1	152	2	T03173	gelatinase homolog
43	57	22.1	351	2	F64880	ycjs protein - esc
44	57	22.1	351	2	C85753	probable dehydroge
45	57	22.1	351	2	F90865	probable dehydroge

#### ALIGNMENTS

##### RESULT 1

KCHUS1

stromelysin 1 (EC 3.4.24.17) precursor [validated] - human

N:Alternate names: angiotatin-converting enzyme; collagenase activating protein; matrilysin

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1992 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C:Accession: A28156; C29157; A28399; A60964; S15427

R:Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.

J. Biol. Chem. 263, 6742-6745, 1988

A:Title: The complete primary structure of human matrix metalloproteinase-3. Identity w

A:Reference number: A28156; MUID:88198243; PMID:3360803

A:Accession: A28156

A:Molecule type: mRNA

A:Residues: 1-44, 'E', '46-477 <SAU>

A:Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G18861

R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris

Biochem. J. 240, 913-916, 1986

A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analys

A:Reference number: A90336; MUID:87158645; PMID:3030290

A:Accession: C29157

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-477 <WHI>

A:Cross-references: ENBL:X05232; NID:G36632; PIDN:CAA38859.1; PID:G36633

R:Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisen, A.Z.; Warner, B.L.; Grant, G.A.;

Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987

A:Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specifi

A:Reference number: A28399; MUID:88016164; PMID:3477804

A:Accession: A28399

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-49, 'G', '51-419, 'L', '421-477 <WIL>

A:Cross-references: GB:U78045; NID:G1688257; PIDN:AAB36942.1; PID:G1688259

A>Note: part of the sequence, including the amino end of the proenzyme, was confirmed b

R:Lark, M.W.; Walakowits, L.A.; Shah, T.K.; Vanniddlesworth, J.; Cameron, P.M.; Lin, T.

Connect. Tissue Res. 25, 49-65, 1990

A:Title: Production and purification of prostromelysin and procollagenase from IL-1 bet

A:Reference number: A60964; MUID:91059606; PMID:2173990

A:Accession: A60964

A:Molecule type: protein

A:Residues: 18-29,100-108 <LAR>

R:Kokitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.

Biochem. J. 276, 217-221, 1991

A:Title: Purification of recombinant human prostromelysin. Studies on heat activation t

A:Reference number: S15427; MUID:91248150; PMID:2039471

A:Accession: S15427

A:Status: preliminary

A:Molecule type: protein

A:Residues: 18-23 <BIO>

R:Lipinen, H.R.; Ugwu, F.; Bini, A.; Collen, D.

Biochemistry 37, 4699-4702, 1998

```

ed with collagenase.
A:Reference number: A3706; MUID:89077214; PMID:2825726
A:Accession: A37306
A:Molecule type: mRNA
A:Residues: 1-478 <FN>
A:Cross-references: UNIPROT:P28863; GB:M25664; NID:g165709; PIDN:AAA31467.1; PID:g165710; B.E.Cham. J. 240, 913-916, 1986
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris, E.
A>Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A:Reference number: A90336; MUID:87156645; PMID:3030290
A:Accession: A29157
A:A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-82,'D','84'-127,'K','129-167','GNS','>WHI>'
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin. Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with catalytic activity. Stromelysin 1 activates its proenzyme after cleavage(s) within the activation site. Stromelysin is found in glycosylated and unglycosylated forms, both of which are active.
C:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side of aspartate residues. hemopexin repeat homology; matrix metalloproteinase family. interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase superfamily. extracellular matrix: fibroblast; glycoprotein; hydrolase; metallopeptidase. calcium; extracellular matrix: fibroblast; glycoprotein; hydrolase; metallopeptidase. signal sequence #status predicted <SIG>
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-478/Product: prostromelysin 1 #status predicted <PRO>
F:18-100/Domain: activation peptide #status predicted <ACT>
F:61-265/Domain: matrix metalloproteinase homology <MMP>
F:91-98/Region: autoinhibitory
F:101-478/Product: stromelysin 1 #status predicted <MAT>
F:288-478/Domain: hemopexin repeat homology <XPN>
F:93,219,223,229/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:121/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:219,223,229/Binding site: zinc, catalytic (His) (active) #status predicted
F:220/Active site: Glu #status predicted
F:291-478/Dissulfide bonds: #status predicted

Query Match      53.5%; Score 138; DB 1; Length 478;
Best Local Similarity 60.5%; Pred. No. 1.6e-10;
Matches 26; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY          1 LQQLSLPETCELDLSATLKAMRTPCRGVPDLGRFQTFFEGDLKW 43
DB          58 WKFLCLEVTGKLDSNTLEIVRKRCGVDPDVGHFTFGTPKKW 110


RESULT 3
KCRTIH
stomelysin 1 (BC 3.4.24.17) precursor - rat
UNAlternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C:Accession: A00997; PS0150; S22767
R:Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A>Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A:Reference number: A00997; MUID:85284930; PMID:3875482
A:Accession: A00997
A:Molecule type: mRNA
A:Residues: 1-475 <MAL>
A:Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIN:CAA26448.1; PID:G957461
R:Tjener, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A>Title: Purification and properties of extracellular matrix-degrading metallo-proteinases
A:Reference number: PS0150; MUID:91154156; PMID:1963430
A:Accession: PS0150
A:Molecule type: protein
A:Residues: 19-20,'X','22-28,'110-112','X','114-115','X','117','X','119;309-325 <UMB>
R:Breatnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A>Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A:Reference number: A26403; MUID:87146421; PMID:3547333
A:Contents: annotation; introns
A>Note: Intron positions were determined by comparison of the previously reported cDNA s. Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breatnach, R.
```

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F:219/Active site: Glu #status predicted  
F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;  
Best Local Similarity 58.1%; Pred. No. 7.4e-10;  
Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Oy 1 LQKLSLPETGEILSDATLKAWRPRCGVPLGRFTQTEGLKW 43  
:  
Db 66 MQKFLGLEVTGKLDSNTMELMHXPRCGVPDVGGSFPFGPKW 109  
:  
:

RESULT 5  
KCRTS2  
stromelysin 2 (EC 3.4.24.22) precursor [validated] - human  
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A28816; A47496  
R:Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach,  
Biochem. J. 253, 187-192, 1988  
A:Title: The collagenase gene family in humans consists of at least four members.  
A:Reference number: A90339; PMID:88339885; PMID:2844164  
A:Accession: A28816  
A:Molecule type: mRNA  
A:Residues: 1-476 <full>  
A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:936628; PIDN:CMA30679.1; PID:g3662  
A>Note: mRNA for this protein was detected in several human tumors  
R:Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Boddien, M.K.; Engler, J.A.; Birkedal  
J. Biol. Chem. 268, 17341-17347, 1993  
A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 ge  
A:Reference number: A47496; PMID:93352520; PMID:8349617  
A:Accession: A47496  
A:Molecule type: protein  
A:Residues: 17-33 <WTN>  
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
C:Genetics:  
A:Gene: GDB:MMP10; STMY2  
A:Cross-references: GDB:120392; OMIM:185260  
A:Map position: 11q22.3-11q23  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-476/Product: prostromelysin 2 #status experimental <PRO>  
F:17-98/Domain: activation peptide #status predicted <ACT>  
F:59-263/Domain: matrix metalloproteinase homology <MMP>  
F:89-96/Region: autoinhibitory  
F:99-476/Product: stromelysin 2 #status predicted <MAT>  
F:283-476/Domain: hemopexin repeat homology <PXN>  
F:191,217,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F:119/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted  
F:218/Active site: Glu #status predicted  
F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;  
Best Local Similarity 58.1%; Pred. No. 7.4e-10;  
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Oy 1 LQKLSLPETGEILSDATLKAWRPRCGVPLGRFTQTEGLKW 43  
:  
Db 66 MQKFLGLEVTGKLDSNTMELMHXPRCGVPDVGHSFPFGPKW 108  
:  
:

RESULT 6  
KCRTS2  
stromelysin 2 (EC 3.4.24.22) precursor - rat  
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: B26403; A41775; S26498  
R:Breathnach, R.; Marisaisan, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.

Nucleic Acids Res. 15, 1139-1151, 1997

A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A:Reference number: A26403; MUID:87146421; PMID:3547333

A:Accession: B26403

A:Molecule type: mRNA

A:Residues: 1-476 <BRE>

A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57389

A:Note: Intron positions were determined by comparison of the cDNA sequence to genomic

A:Note: mRNA for this protein was expressed in several transformed rat embryo fibroblast

P:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas

J. Biol. Chem. 267, 1099-1103, 1992

A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ

A:Reference number: A41775; MUID:92112748; PMID:1370458

A:Accession: A41775

A:Molecule type: mRNA

A:Residues: 1-476 <CHA>

A:Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151

A:Note: Sequence extracted from NCBI backbone (NCBI:P76184)

R:de Voege, M.W.; Mukherjee, B.B.

Oncogene 7, 109-119, 1992

A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra

A:Reference number: S26496; MUID:92158347; PMID:1741158

A:Accession: S26498

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 31-103, 'L', 241-242, 'TQMEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>

A:Cross-references: EMBL:X64020

C:Genetics:

A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-99/Domain: activation peptide #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Domain: hemopexin repeat homology <PXM>

F:283-476/Domain: hemopexin repeat homology <PXM>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:120/Binding site: carboxylate (Asn) (covalent) #status predicted

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F:219/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 53.2%; Pred. No. 7.4e-10;

Matches 25; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVDPDLGRFQTFEGDLKWHHN 47

DB 67 MQKFLGLEMTGKLDSTNEMHPRCGVDPVGGFSTFPGSPKRNH 113

RESULT 7

KCMSS1

stromelysin 1 (EC 3.4.24.17) precursor - mouse

N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C:Accession: JCI476; S18867; S32963; S33139

R:Hammani, K.; Henriet, P.; Beckhout, Y.

Gene 120, 321-322, 1992

A:Title: Cloning and sequencing of a cDNA encoding mouse stromelysin 1.

A:Reference number: JCI476; MUID:93013057; PMID:1398148

A:Accession: JCI476

A:Molecule type: mRNA

A:Residues: 1-477 <HAM>

A:Cross-references: UNIPROT:P28862; EMBL:X66402; NID:G236167; PIDN:CAA47029.1; PID:G2961

A:Note: It is uncertain whether Wet-1 is the initiator or whether translation is initiat

R:Li, F.; Strange, R.; Saurer, S.; Niemann, H.; Fries, R.R.

submitted to the EMBL Data Library, August 1991

A:Reference number: S18867

A:Accession: S18867

A:Molecule type: mRNA

A:Residues: 'MK', 1-477 <LIF>

A:Cross-references: EMBL:X63162; NID:G54871; PIDN:CAA44860.1; PID:G54872

R:Brenner, C.A.; Adler, R.R.; Rappolee, D.A.; Pedersen, R.A.; Werb, Z.

Genes Dev. 3, 848-859, 1989

A:Title: Genes for extracellular matrix-degrading metalloproteinases and their inhibitor

A:Reference number: A32963; MUID:89306621; PMID:2744464

A:Accession: B32963

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 415-467, 'T', 469 <BRE>

A:Experimental source: clone EMS-2

C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit

C:Comment: Stromelysin is found in glycosylated and unglycosylated forms, both of whi

C:Function: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-99/Domain: activation peptide #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-477/Domain: hemopexin repeat homology <PXM>

F:284-477/Domain: hemopexin repeat homology <PXM>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

F:219/Active site: Glu #status predicted

F:290-477/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 477;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVDPDLGRFQTFEGDLK 43

DB 67 MQKFLGLEMTGKLDSTNEMHPRCGVDPVGGFSTFPGSPK 109

RESULT 8

S29243

Interstitial collagenase (EC 3.4.24.7) precursor - mouse

N:Alternate names: matrix metalloproteinase 1 (MMP1)

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004

C:Accession: S29243

R:Henriet, P.; Rousseau, G.G.; Beckhout, Y.

FEBS Lett. 310, 175-178, 1992

A:Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat c

A:Reference number: S29243; MUID:93011910; PMID:1383028

A:Accession: S29243

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-472 <HEN>

A:Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G53604

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:65-268/Domain: matrix metalloproteinase homology <MMP>

F:279-472/Domain: hemopexin repeat homology <PXM>

F:97,223,227,233/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted

F:224/Active site: Glu #status predicted

Query Match 46.9%; Score 121; DB 2; Length 472;

Best Local Similarity 48.9%; Pred. No. 3e-08;

Matches 23; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRPRCGVDPDLGRFQTFEGDLKWHHN 47

DB 72 MQSPFGLVETGKLDPTLDIMKPRCGVDPVGGFSTFRTLKWSQTN 118

```

RESULT 9
A23685
N;Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C;Accession: A23685
R;Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge
J. Biol. Chem. 265, 22342-22347, 1990
A;Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone
A;Reference number: A23685; MUID:91039077; PMID:2176215
A;Accession: A23685
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <QUI>
A;Cross-references: UNIPROT:P23097; GB:M60616; NID:G203498; PIDN:AAA72124.1;
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;59-262/Domain: matrix metalloproteinase homology <MMP>
F;273-466/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted

Query Match 45.7%; Score 118; DB 2; Length 466;
Best Local Similarity 48.9%; Pred. No. 7.5e-08;
Matches 23; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTRPCGVDPDLGRFQTFEGDLKWHN 47
DB 66 MQSFFGLDVTGKLDLDFDLMRRCGVDPDVGYNVFPRTLKWSQIN 112

RESULT 10
A53711
collagenase 3 (EC 3.4.24.-) - human
N;Alternate names: matrix metalloproteinase 13 (MMP13)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53711
R;Freije, J.M.P.; Diez-Itza, I.; Balbin, M.; Sanchez, L.M.; Blasco, R.; Toliwia, J.; Lopez
J. Biol. Chem. 269, 16766-16773, 1994
A;Title: Molecular cloning and expression of collagenase-3, a novel human matrix metallo
A;Reference number: A53711; MUID:94266894; PMID:8207000
A;Accession: A53711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <PRE>
A;Cross-references: UNIPROT:P45452; GB:X75308; NID:G516385; PIDN:CAA53056.1; PID:G516386
C;Genetics:
A;Gene: GDB:MMP13; CLG3
A;Cross-references: GDB:373966; OMIM:600108
A;Map position: 11q22.2-11q22.3
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;64-267/Domain: matrix metalloproteinase homology <MMP>
F;278-471/Domain: hemopexin repeat homology <PXN>
F;96,222,226,232/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
F;223/Active site: Glu #status predicted

Query Match 45.3%; Score 117; DB 2; Length 471;
Best Local Similarity 46.8%; Pred. No. 1e-07;
Matches 22; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTRPCGVDPDLGRFQTFEGDLKWHN 47
DB 71 MQSFFGLDVTGKLDLDFDLMRRCGVDPDVGYNVFPRTLKWSQIN 117

RESULT 11
A57490
matrilysin (EC 3.4.24.23) precursor - rat
N;Alternate names: matrix metalloproteinase 7 (MMP7)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57490
R;Abramson, S.R.; Conner, G.E.; Nagase, H.; Neuhaus, I.; Woessner Jr., J.F.
J. Biol. Chem. 270, 15016-15022, 1995
A;Title: Characterization of rat urokinase matrilysin and its cDNA. Relationship to human
A;Reference number: A57490; MUID:95332299; PMID:7608162
A;Accession: A57490
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <ABR>
A;Cross-references: UNIPROT:P50280; GB:L24374; NID:G402492; PIDN:AAA93432.1; PID:G402492
C;Superfamily: matrilysin; matrix metalloproteinase homology
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-267/Domain: signal sequence #status predicted <SIG>
F;58-262/Domain: matrix metalloproteinase homology <MMP>
F;90,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted

Query Match 45.0%; Score 116; DB 2; Length 267;
Best Local Similarity 45.5%; Pred. No. 7.4e-08;
Matches 20; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTRPCGVDPDLGRFQTFEGDLKWH 44
DB 65 MQKFFGLPDTGKLSRVMKRCGVDPDVAEFLMNPSPKWH 108

RESULT 12
A28153
Gelatinase A (EC 3.4.24.24) precursor - human
N;Alternate names: collagenase type IV; matrix metalloproteinase 2 (MMP2); progelatinas
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1989 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A28153; A34202; A42225; A60187; S13858; S39436; A31480; S44432; A61498; S5
R;Collier, I.E.; Wilhelm, S.M.; Eisen, A.Z.; Marmer, B.L.; Grant, G.A.; Seltzer, J.L.;
J. Biol. Chem. 263, 6579-6587, 1988
A;Title: H-ras oncogene-transformed human bronchial epithelial cells (TBE-1) secrete a
A;Reference number: A28153; MUID:88198218; PMID:2834383
A;Accession: A28153
A;Molecule type: mRNA
A;Residues: 30-660 <COL>
A;Cross-references: UNIPROT:P08253; GB:J03210; NID:G180670; PIDN:AAA35701.1; PID:G18067
R;Huhtala, P.; Eddy, R.L.; Fan, Y.S.; Byers, M.G.; Shows, T.B.; Tryggvason, K.
Genomics 6, 554-559, 1990
A;Title: Completion of the primary structure of the human type IV collagenase preproenz
A;Reference number: A34202; MUID:90228972; PMID:2158484
A;Accession: A34202
A;Molecule type: DNA
A;Residues: 1-51 <HU2>
A;Cross-references: GB:M33789; NID:G180600; PIDN:AAA52027.1; PID:G180601
R;Huhtala, P.; Chow, L.T.; Tryggvason, K.
J. Biol. Chem. 265, 11077-11082, 1990
A;Title: Structure of the human type IV collagenase gene.
A;Reference number: A42225; MUID:90293047; PMID:2162831
A;Accession: A42225
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-51;220-393 <HUH>
A;Cross-references: GB:IM5593; GB:J05471; NID:G180614; PIDN:AAA52028.1; PID:G180616
A;Note: neither the complete amino acid nor the complete nucleotide sequence is given i
R;Frisch, S.M.; Reich, R.; Collier, I.E.; Genrich, L.T.; Martin, G.; Goldberg, G.I.
Oncogene 5, 75-83, 1990
A;Title: Adenovirus E1A represses protease gene expression and inhibits metastasis of h
A;Reference number: A60187; MUID:90206614; PMID:2157183
A;Accession: A60187
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-58 <PRI>

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Db 77 MQKFFGLPQTGDDLDQNTIETMRXPRCGNPDVANYNFFPRKPKW 119

RESULT 13

A4999  
metalloelastase HME (EC 3.4.24.-) - human  
C/Species: Homo sapiens (man)  
C/Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A49499  
R/Shapiro, S.D.; Kobayashi, D.K.; Levy, T.J.  
J. Biol. Chem. 268, 23824-23829, 1993  
A/Title: Cloning and characterization of a unique elastolytic metalloproteinase produced  
A/Reference number: A49499; MUID:94043200; PMID:8226919  
A/Accession: A49499  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-470 <SHA>  
A/Cross-references: UNIPROT:P39900; GB:I23808; NID:G435969  
A/Experimental source: alveolar macrophage  
A/Note: Sequence extracted from NCBI backbone (NCBIN:139457, NCBI:P139458)  
C/Genetics:  
A/Gene: GDB:MMP12; HME  
A/Cross-references: GDB:266582; OMIM:601046  
A/Map position: 11q22.2-11q22.3  
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase  
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F/60-263/Domain: matrix metalloproteinase homology <MMP>  
F/276-470/Domain: hemopexin repeat homology <PXN>  
F/92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F/218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F/219/Active site: Glu #status predicted

Query Match 43.8%; Score 113; DB 2; Length 470;  
Best Local Similarity 45.7%; Pred. No. 3.5e-07;  
Matches 21; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 LOKQLSLPRTGTGLDSATLKAMTRPCGVPDLGRQFTFGDLKWHH 46

Db 67 MQHFLGLKVTGQLDSTLEWHAPRCGVPDVHFRMPGPGVWRKH 112

RESULT 14

KCHUI  
interstitial collagenase (EC 3.4.24.7) precursor [validated] - human  
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C/Species: Homo sapiens (man)  
C/Date: 13-Aug-1986 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C/Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S2  
R/Temperton, N.S.; Brown, P.D.; Levy, A.J.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St  
Cancer Res. 50, 5431-5437, 1990  
A/Title: Cloning and characterization of human tumor cell interstitial collagenase.  
A/Reference number: A37308; MUID:90352587; PMID:2167156  
A/Accession: A37308  
A/Molecule type: mRNA  
A/Residues: 1-469 <TEM>  
A/Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126  
R/Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.  
J. Clin. Invest. 79, 542-546, 1987  
A/Title: Molecular cloning of human synovial cell collagenase and selection of a single  
A/Reference number: S22766; MUID:87109799; PMID:3027129  
A/Accession: S22766  
A/Molecule type: DNA  
A/Residues: 1-63,65-70 <BRI>  
A/Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667  
R/Angel, P.; Baumann, I.; Stein, B.; Dellius, H.; Rahmsdorf, H.J.; Herrlich, P.  
Mol. Cell. Biol. 7, 2256-2266, 1987  
A/Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene i  
A/Reference number: I57620; MUID:87257941; PMID:3037355  
A/Accession: I57620  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-35 <RES>  
A/Note: translated from GB/EMBL/DBJ



```

A;Cross-references: GDB:119783; OMIM:120353
A;Map position: 11q22.2-11q22.3
C;Function:
C;Superfamily: hydrolyzes collagens, in particular types I, II, III, and X, serpins, an
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-469/Product: procollagenase #status experimental <PRO>
F;20-99/Domain: activation peptide #status experimental <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MWP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status experimental <MAT>
F;172-466/Domain: hemopexin repeat homology <PXN>
F;92, 218, 222, 228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;120, 143/Binding site: carboxylate (Asn) (covalent) #status predicted
F;218, 228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F;278-466/Disulfide bonds: #status experimental

Query Match 42.6%; Score 110; DB 1; Length 469;
Best Local Similarity 46.5%; Pred. NO. 8.9e-07;
Matches 20; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMETPRCGVPDILGRFQTFFGDLKX 43
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 MQEFGELKVTGRPDATLTKVMKQRCGVPDVAQFVLTEGNPRW 109

RESULT 15
PW0052
pro-matrix metalloproteinase-3 - human (fragment)
N;Alternate names: proMMP-3
C;Species: Homo sapiens (man)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PW0052
R;Towle, C.A.; Wright, M.; Hecht, A.C.; Kuong, S.J.; Papanicolas, L.E.; Totkovic, R.; M
Biochem. Biophys. Res. Commun. 247, 324-331, 1998
A;Title: A matrix metalloproteinase proenzyme activator produced by articular cartilage
A;Reference number: PW0052; PMID:98308115; PMID:9642125
A;Accession: PW0052
A;Molecule type: protein
A;Residues: 1-82 <TOW>
C;Comment: This matrix enzyme is involved in connective tissue turnover under physiologi
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote

Query Match 41.9%; Score 108; DB 2; Length 82;
Best Local Similarity 65.6%; Pred. NO. 2.3e-07;
Matches 21; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMETPRCGVPDILG 32
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 50 MQKFLGLEVTGLKLDSDTLEVMKPRCGVPDVG 81

Search completed: November 15, 2004, 14:07:18
Job time : 11.5449 secs

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Search completed: November 15, 2004, 14:07:18  
Job time : 11.5449 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 43.3846 Seconds  
(without alignments)  
623.323 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQKQLSLPETGELDSATLKAA.....VPLDGRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1606865

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	226	87.6	324	Q9N282	Q9N282 bos taurus
2	216	83.7	149	Q9TVB4	Q9TVB4 canis famil
3	141	54.7	477	MM03_HUMAN	P08254 homo sapien
4	141	54.7	477	AAH69676	AAH69676 homo sapi
5	141	54.7	477	AAH69716	AAH69716 homo sapi
6	138	53.5	478	MM03_RABIT	P28863 coryctolag
7	135	52.3	145	Q9N283	Q9N283 bos taurus
8	134	51.9	475	MM03_RAT	P03957 rattus norv
9	133	51.6	139	Q9GM68	Q9GM68 sus scrofa
10	133	51.6	476	MM10_HUMAN	P09238 homo sapien
11	133	51.6	476	MM10_MOUSE	O55123 mus musculu
12	133	51.6	476	MM10_RAT	P07152 rattus norv
13	133	51.6	476	AAH36110	AAH36110 homo sapi
14	133	51.6	477	MM03_MOUSE	P28862 mus musculu
15	133	51.6	479	Q922M6	Q922M6 mus musculu
16	131	50.8	478	Q6Y4Q5	Q6Y4Q5 canis famil
17	131	50.8	478	AAO3580	AAO3580 canis fam
18	128	49.6	167	Q7ZWD0	Q7ZWD0 brachydanio
19	128	49.6	465	MM08_MOUSE	Q8C209 mus musculu
20	128	49.6	465	Q8C209	Q8C209 mus musculu
21	128	49.6	465	Q8C230	Q8C230 mus musculu
22	128	49.6	465	AAH42742	AAH42742 mus muscu
23	128	49.6	465	BAC40805	BAC40805 mus muscu
24	128	49.6	466	MM08_RAT	O88766 rattus norv
25	128	49.6	475	Q71G59	Q71G59 brachydanio
26	128	49.6	475	AAQ07962	AAQ07962 brachydan
27	127	49.2	393	Q8MI18	Q8MI18 felis silve
28	126	48.8	657	Q7SZM5	Q7SZM5 brachydanio
29	126	48.8	657	Q6DG10	Q6DG10 brachydanio
30	124	48.1	223	Q7TOK9	Q7TOK9 ambystoma m
31	124	48.1	252	Q6PWQ3	Q6PWQ3 xenopus lae

32	124	48.1	252	2	AA00547	AA00547 xenopus lae
33	124	48.1	259	2	Q7ZTI9	Q7ZTI9 xenopus lae
34	124	48.1	657	2	Q9PTU7	Q9PTU7 oryzias lat
35	123	47.7	477	1	MM03_HORSE	Q2837 equus cabal
36	122	47.3	259	2	Q6DF35	Q6DF35 xenopus tro
37	121	46.9	471	2	Q98859	Q98859 cynops pyrr
38	121	46.9	472	1	MM13_MOUSE	P3435 mus musculu
39	120	46.5	126	2	Q9TT84	Q9TT84 sus scrofa
40	120	46.5	632	2	Q9NIP6	Q9NIP6 canis famil
41	119	46.1	655	2	Q9W635	Q9W635 oncorhynch
42	118	45.7	466	1	MM13_RAT	P2307 rattus norv
43	117	45.3	121	2	Q6LBE5	Q6LBE5 homo sapien
44	117	45.3	121	2	CAA57296	CAA57296 homo sapi
45	117	45.3	383	2	Q7Z5M0	Q7Z5M0 homo sapien

ALIGNMENTS

RESULT 1

Q9N282 ID Q9N282 PRELIMINARY; PRT; 324 AA.  
AC Q9N282; 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE MRP-9 (Fragment).  
GN Name=brmp-9;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
[1]  
SEQUENCE FROM N.A.  
RA Sato T., Hirata M., Ito A., Hashizume K.;  
BL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB043996; BAA96389.1;  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000562; FN Type II.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR Pfam; PF00040; fn2; 2.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase M10\_N; 1.  
DR PRINTS; PR00013; FNYPEII.  
DR PRINTS; PR00138; MATRINX.  
DR ProDom; PD000995; FN Type II; 2.  
DR SMART; SM00059; FN2\_2.  
DR SMART; SM00235; ZnMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00023; FIBRONECTIN\_2; 1.  
FT NON TER 324 324  
SQ SEQUENCE 324 AA; 36273 MW; 4137C9820C28E080 CRC64;

Query Match 87.6%; Score 226; DB 2; Length 324;

Best Local Similarity 84.8%; Pred. No. 2.8e-22; Mismatches 3; Indels 0; Gaps 0;  
Matches 39; Conservative 4;

QY 2 QKQLSLPETGELDSATLKAMRTPRCGVFDLGRFQTFEGDLKWHHN 47  
DB 75 QRRSLRPETGELDTTLNAMRAPCGVFDVGRFQTFEGDLKWHHN 120

RESULT 2

Q9TVB4 ID Q9TVB4 PRELIMINARY; PRT; 149 AA.  
AC Q9TVB4; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)

DE Type IV collagenase MMP-9 (Fragment).  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibrosarcoma;  
RA Paria B.C., Kitchell B.E.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF1471104; AAD31323.1;  
DR GO; GO:0005708; C:extracellular matrix; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR005070; PGSD like.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase M10\_N; 1.  
DR PRINTS; PR00138; MATRXIN.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
KW Collagen.  
FT NON\_TER 149 149  
SQ SEQUENCE 149 AA; 17025 MW; CAGA5062EFDCCBBF CRC64;  
Query Match 83.7%; Score 216; DB 2; Length 149;  
Best Local Similarity 78.7%; Pred. No. 2.7e-21;  
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LKQLSLPTGELDSATLKAMTPRCGVDPDLGRFQTFEGDLKWHHN 47  
DB 74 LQRLALPETGELDKTLEAMRAPRCGVDPDLGKFTQTFEGDLKWHND 120  
RESULT 3  
MM03\_HUMAN  
ID MM03\_HUMAN STANDARD; PRT; 477 AA.  
AC P08254;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)  
DE (MMP-3) (Transin-1) (SL-1).  
GN Names=MMP3; Synonyms=STMY1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.  
RX MEDLINE=88198243; PubMed=3360803;  
RA Saus J., Quinones S., Orani Y., Nagase H., Harris E.D. Jr.,  
RA Kurkinen M.;  
RT "The complete primary structure of human matrix metalloproteinase-3.  
RT Identity with stromelysin.";  
RL J. Biol. Chem. 263:6742-6745(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=87156645; PubMed=3030290;  
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,  
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
RT "Comparison of human stromelysin and collagenase by cloning and  
RT sequence analysis.";  
RL Biochem. J. 240:913-916(1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88016164; PubMed=3477804;  
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,  
RA Grant G.A., Bauer E.A., Goldberg G.I.;  
RT "Human skin fibroblast stromelysin: structure, glycosylation, and  
RT substrate specificity, and differential expression in normal and  
RT tumorigenic cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729(1987).  
RN [12]  
RN SEQUENCE FROM N.A.  
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
RA Heller R., Davis R.W.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RT "SeattlesNPs: NHLBI HL66682 program for genomic applications, UW-  
RT FHCRC Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP ZYMOGEN ACTIVATION.  
RX MEDLINE=90344802; PubMed=2383557;  
RA Nagase H., Englund J.J., Suzuki K., Salvesen G.;  
RT "Stepwise activation mechanisms of the precursor of matrix  
RT metalloproteinase 3 (stromelysin) by proteinases and (4-  
RT aminophenyl)mercuric acetate.";  
RL Biochemistry 29:5783-5789(1990).  
RN [7]  
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.  
RX MEDLINE=95384761; PubMed=7656014;  
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,  
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,  
RA Johnson B.A.;  
RT "The NMR structure of the inhibited catalytic domain of human  
RT stromelysin-1.";  
RL Nat. Struct. Biol. 1:111-118(1994).  
RN [8]  
RP STRUCTURE BY NMR OF 100-267.  
RX MEDLINE=99043696; PubMed=9827994;  
RA Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A.,  
RA Kloosterman D.A., Mizeak S.A., Jacobsen E.J., Belonga K.L.,  
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,  
RA Ledbetter S.R., Kaytes P.S., Vogeli G., Marshall V.P., Petzold G.L.,  
RA Poorman R.A.;  
RT "Solution structures of stromelysin complexed to thiadiazole  
RT inhibitors.";  
RL Protein Sci. 7:2281-2286(1998).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.  
RX MEDLINE=96117647; PubMed=8535233;  
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,  
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,  
RA Hermes J.D., Springer J.P.;  
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic  
RT domain and of the C-truncated proenzyme.";  
RL Protein Sci. 4:1966-1976(1995).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.  
RX MEDLINE=96311273; PubMed=8740360;  
RA Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.F.,  
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;  
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin  
RT catalytic domain and its comparison with members of the zinc  
RT metalloproteinase superfamily.";  
RL Structure 4:375-386(1996).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.  
RX MEDLINE=97236985; PubMed=9083493;  
RA Esser C.K., Bugianesi R.B., Caldwell C.G., Chapman K.T., Durette P.L.,  
RA Girotta N.N., Kopka I.E., Lanza T.J., Levorse D.A., Maccoss M.,  
RA Owens K.A., Pompidom M.M., Simeone J.P., Harrison R.K.,  
RA Niedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,  
RA McDowell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M.,  
RA Shen F., Colletti A., Krieter P.A., Hagmann W.K.;  
RT "Inhibition of stromelysin-1 (MMP-3) by Fl'-biphenylylethyl  
RT carboxylalkyl dipeptides.";  
RL J. Med. Chem. 40:1026-1040(1997).  
RN [12]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH  
TMPL.  
RX MEDLINE=97433330; PubMed=9288970;  
RA Gomis-Rueh F.-X., Maskos K., Betz M., Bergner A., Huber R.,  
RA Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,  
RA Bartunik H., Bode W.,  
RT "Mechanism of inhibition of the human matrix metalloproteinase  
stromelysin-1 by TIMP-1.",  
RL Nature 389:77-81(1997).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.  
RX MEDLINE=99006562; PubMed=9792098;  
RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,  
RA Trepoed C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A.,  
RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.,  
RT "Structural characterizations of nonpeptidic thiazole inhibitors of  
matrix metalloproteinases reveal the basis for stromelysin  
selectivity.",  
RL Protein Sci. 7:2118-2126(1998).  
RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.  
RX MEDLINE=20013087; PubMed=10543949;  
RA Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M.,  
RA Barnett B.L.,  
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A  
resolution: inhibitor-induced conformational changes.",  
RL J. Mol. Biol. 293:545-557(1999).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.  
RX MEDLINE=99349695; PubMed=10422833;  
RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwin D.F.,  
RA Purchase C.F. II, White A.D., Dhanraj V., Roth B.D., Johnson L.L.,  
RA Hupe D., Humblet C., Blundell T.L.,  
RT "X-ray structure of human stromelysin catalytic domain complexed with  
nonpeptide inhibitors: implications for inhibitor selectivity.",  
RL Protein Sci. 8:1455-1462(1999).  
RN [16]  
RP STRUCTURE BY NMR OF 100-272.  
RX MEDLINE=98434377; PubMed=9760240;  
RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.,  
RT "Solution structure of the catalytic domain of human stromelysin-1  
complexed to a potent, nonpeptidic inhibitor.",  
RL Biochemistry 37:14048-14056(1998).  
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,  
CC III, IV, and V; collagens III, IV, X, and IX, and cartilage  
CC proteoglycans. Activates procollagenase.  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'  
CC are hydrophobic residues.  
CC -!- COPACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X05232; CAA28859.1; -  
DR ENBL; J03209; AAA36321.1; -  
DR ENBL; U78045; AAB36942.1; -  
DR ENBL; AF405705; AAK95247.1; -  
DR PIR; A28156; KCHU51.  
DR PDB; 1B3D; X-ray; A/B=100-272.  
DR PDB; 1B8Y; X-ray; A=100-266.  
DR PDB; 1BIW; X-ray; A/B=100-272.  
DR PDB; 1BM6; NMR; @=100-272.  
DR PDB; 1BQ0; X-ray; A/B=100-272.  
DR PDB; 1C31; X-ray; A/B=100-272.  
DR PDB; 1C8T; X-ray; A/B=103-269.  
DR PDB; 1CAQ; X-ray; A=100-267.

DR PDB; 1CIZ; X-ray; A=100-267.  
DR PDB; 1CQR; X-ray; A/B=100-272.  
DR PDB; 1D5J; X-ray; A/B=100-272.  
DR PDB; 1D7X; X-ray; A/B=100-272.  
DR PDB; 1D8F; X-ray; A/B=100-272.  
DR PDB; 1D8M; X-ray; A/B=100-272.  
DR PDB; 1G05; X-ray; A/B=100-272.  
DR PDB; 1G49; X-ray; A/B=100-272.  
DR PDB; 1G4K; X-ray; A/B/C=100-267.  
DR PDB; 1HFS; X-ray; @=105-264.  
DR PDB; 1HY7; X-ray; A/B=100-272.  
DR PDB; 1M1W; Model; A=100-268.  
DR PDB; 1M09; NMR; A=100-267.  
DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.  
DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.  
DR PDB; 1SLM; X-ray; @=18-272.  
  
Query Match 54.7%; Score 141; DB 1; Length 477;  
Best Local Similarity 62.8%; Pred. No. 1.9e-10;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 LOKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKW 43  
DB 67 MQKFLGLEVTGKLDSTLVNKRPGVDPVGHFRTPFGIPKW 109  
  
RESULT 4  
AAH659676 PRELIMINARY; PRT; 477 AA.  
AC AAH69676;  
DT 20-MAY-2004 (TrEMBLrel. 27, Created)  
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
DE Matrix metalloproteinase 3, preproprotein.  
CN MRP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PCR rescued clones;  
RX MEDLINE=2238825; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marz M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PCR rescued clones;  
RA Strausberg R.;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC069676; AAH69676.1; -  
SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEEA9 CRC64;  
  
Query Match 54.7%; Score 141; DB 2; Length 477;  
Best Local Similarity 62.8%; Pred. No. 1.9e-10;





DT	01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE	Matrix metalloproteinase-3 (Fragment).
GN	Name=MMP-3;
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Kanaki T., Bujo H., Mori S., Takahashi K., Yokote K., Morisaki N.,
RA	Saito Y.;
RL	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AB044413; BAB16112.1; -.
DR	MEROPS; M10.005; -.
DR	GO; GO:0005578; C:extracellular matrix; IEA.
DR	GO; GO:0004222; P:metalloendopeptidase activity; IEA.
DR	GO; GO:006508; P:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR006026; Peptidase M.
DR	InterPro; IPR001818; Pept_M10A_M12B.
DR	Pfam; PF00413; Peptidase_M10; 1.
DR	Pfam; PF03933; Peptidase_M10_N; 1.
DR	PRINTS; PR00138; MATRIXIN.
DR	SMART; SM00235; ZnMG; 1.
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.
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	Matches 26; Conservative 6; Mismatches 15; Indels 0; Gaps
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RESULT 10	
MM10_HUMAN	
ID	MM10_HUMAN STANDARD; PRT; 476 AA.
AC	F09338;
CD	01-MAR-1989 (Rel. 10, Created)
DT	01-MAR-1989 (Rel. 10, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE	(MMP-10) (Transin-2) (SL-2).
GN	Name=MMP10; Synonyms=STM2;
CS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89339885; PubMed=2844164;
RA	Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.J.,
RA	Breathnach R.;
RT	"The collagenase gene family in humans consists of at least four
RT	members.";
RL	Biochem. J. 253:187-192(1988).
RL	[2]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Ovary;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA	Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,





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CC EMBL; Y13185; CAA73641.1; -.  
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 CC HSP; P08254; IG05.  
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 CC InterPro; IPR001818; Pept\_M10A\_M12B.  
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 CC Pfam; PF03933; Peptidase M10\_N; 1.  
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 CC SMART; SM00235; ZnMc; 1.  
 CC PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 CC PROSITE; PS00024; HEMOPEXIN; 1.  
 CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
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 CC PROPP 18 99 Activation peptide (By similarity).  
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 CC DOMAIN 286 476 Hemopexin-like.  
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 CC METAL 218 218 Zinc (catalytic) (By similarity).  
 CC ACT\_SITE 219 219 By similarity.  
 CC METAL 222 222 Zinc (catalytic) (By similarity).  
 CC METAL 228 228 Zinc (catalytic) (By similarity).  
 CC DISULFID 289 476 By similarity.  
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 CC Query Match 51.6%; Score 133; DB 1; Length 476;  
 CC Best Local Similarity 58.1%; Pred. No. 2.4e-09;  
 CC Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
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 CC Db 67 MQKFLGLEMTGKLDSTNTELMKPRCGVDPVGVGFSTFGSPKRW 109  
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 CC AC P07152;  
 CC DT 01-APR-1988 (Rel. 07, Created)  
 CC DT 01-APR-1988 (Rel. 07, Last sequence update)  
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)  
 CC DE (MMP-10) (Transin-2) (SL-2) (transformation-associated protein 34A).  
 CC GN Name=Mmp10;  
 CC OS Rattus norvegicus (Rat).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC OX NCBI\_TaxID=10116;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=87146421; PubMed=3547333;  
 CC RA Breathnach R., Matrisian L.M., Gesnel M.-C., Staub A., Leroy P.;  
 CC RT "Sequences coding for part of oncogene-induced transin are highly  
 CC RL conserved in a related rat gene."  
 CC RL Nucleic Acids Res. 15:1139-1151(1987).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE=92112748; PubMed=1370458;

Chan J.C., Scanlon M., Zhang H.Z., Jia L.B., Yu D., Hung M.C.,  
 French M., Eastman E.M.;  
 "Molecular cloning and characterization of v-mos-activated  
 transformation-associated proteins.";  
 J. Biol. Chem. 267:1099-1103(1992).  
 CC -!- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,  
 CC and V, weakly collagens III, IV, and V. Activates procollagenase.  
 CC -!- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on  
 CC collagen types III, IV and V is weak.  
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC  
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 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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CC EMBL; X05083; CAA28739.1; -.  
 CC EMBL; M65253; AAA42202.1; -.  
 CC PIR; B26403; KCRTS2.  
 CC HSP; P08254; IHY7.  
 CC MEROPS; M10.006; -.  
 CC RGD; 620192; Mmp10.  
 CC InterPro; IPR000585; Hemopexin.  
 CC InterPro; IPR006026; Peptidase M.  
 CC InterPro; IPR001818; Pept\_M10A\_M12B.  
 CC InterPro; IPR006025; Pept\_M10A\_BS.  
 CC InterPro; IPR009070; PGSD\_like.  
 CC Pfam; PF00045; Hemopexin; 4.  
 CC Pfam; PF00413; Peptidase M10; 1.  
 CC Pfam; PF03933; Peptidase M10\_N; 1.  
 CC PRINTS; PR00138; MATRIXIN.  
 CC SMART; SM00120; HX; 4.  
 CC SMART; SM00235; ZnMc; 1.  
 CC PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 CC PROSITE; PS00024; HEMOPEXIN; 1.  
 CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;  
 CC Metalloprotease; Signal; Zinc; Zymogen.  
 CC SIGNAL 1 17 Probable.  
 CC PROPP 18 99 Activation peptide (By similarity).  
 CC CHAIN 100 476 Stromelysin-2.  
 CC DOMAIN 286 476 Hemopexin-like.  
 CC SITE 92 92 Cysteine switch (By similarity).  
 CC METAL 218 218 Zinc (catalytic) (By similarity).  
 CC ACT\_SITE 219 219 By similarity.  
 CC METAL 222 222 Zinc (catalytic) (By similarity).  
 CC METAL 228 228 Zinc (catalytic) (By similarity).  
 CC DISULFID 289 476 By similarity.  
 CC SEQUENCE 476 AA; 54221 MW; B556B6FB1D8BA7EE CRC64;  
 CC  
 CC Query Match 51.6%; Score 133; DB 1; Length 476;  
 CC Best Local Similarity 53.2%; Pred. No. 2.4e-09;  
 CC Matches 25; Conservative 7; Mismatches 15; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LQKQLSLPTGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47  
 CC Db 67 MQKFLGLEMTGKLDSTNTELMKPRCGVDPVGVGFSTFGSPKRWKH 113  
 CC  
 CC RESULT 13  
 CC AAP36110  
 CC ID AAP36110 PRELIMINARY; PRT; 476 AA.  
 CC AC AAP36110;  
 CC DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 CC DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 CC DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 CC DE Matrix metalloproteinase 10 (Stromelysin 2).  
 CC OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_SEQUENCE FROM N.A.  
RP Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
RT vector";  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDIJ databases.  
DR EMBL; BT007442; AAP36110.1; -- 516CDDFF92A0D6 CRC64;  
SQ SEQUENCE 476 AA; 54151 MW; 516CDDFF92A0D6 CRC64;  
  
Query Match 51.6%; Score 133; DB 2; Length 476;  
Best Local Similarity 58.1%; Pred. No. 2.4e-09;  
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 LQKQSLPTGELDNTLKAMTPTGCVDPDLGRFOTFGDLKW 43  
DB 66 MQKFLGLEVTGKLDITLLEWVRKPRGVPDVGHFSFGMPKW 108  
  
RESULT 14  
MM03 MOUSE  
ID MM03 MOUSE STANDARD; PRT; 477 AA.  
AC P28862;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)  
DE (MMP-3) (Transin-1) (SL-1) (EMS-2).  
GN Name=Mmp3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Calvaria;  
RX MEDLINE=93013057; PubMed=1398148;  
RA Hammani K., Henriot P., Beckhout Y.;  
RT "Cloning and sequencing of a cDNA encoding mouse Stromelysin 1.";  
RL Gene 120:321-322(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Swiss;  
RA Li F., Strange R., Saurer S., Niemann H., Friis R.R.;  
RL Submitted (AUG-1991) to the EMBL/GenBank/DDIJ databases.  
RN [3]  
RP SEQUENCE OF 415-469 FROM N.A., AND DEVELOPMENTAL STAGE.  
RX PubMed=2744464;  
RA Brenner C.A., Adler R.R., Rappolee D.A., Pedersen R.A., Werb Z.;  
RT "Genes for extracellular-matrix-degrading metalloproteinases and their  
inhibitor, TIMP, are expressed during early mammalian development.";  
RL Genes Dev. 3:848-859(1989).  
CC CC -1- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,  
III, IV, and V; collagens III, IV, X, and IX, and cartilage  
proteoglycans. Activates procollagenase.  
CC CC -1- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'  
are hydrophobic residues.  
CC CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By  
similarity).  
CC CC -1- DEVELOPMENTAL STAGE: Present in unfertilized eggs and at the  
zygote and cleavage stages. Levels increase at the blastocyst  
stage and with endoderm differentiation.  
CC CC -1- SIMILARITY: Belongs to peptidase family M10A.  
CC CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
CC  
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CC -----  
DR EMBL; X66402; CAA47029.1; --  
DR EMBL; X63162; CAA44860.1; ALT\_INIT.  
DR PR; JCI476; KCMSS1.  
DR HSSP; P08254; IG05.  
DR MEROPS; M10.005; --  
DR MGD; MGI:97010; Mmp3.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase\_M.  
DR InterPro; IPR001843; Pept\_M10A\_M10C.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR009070; PGBD\_like.  
DR Pfam; PF02051; Fragilysin; 1.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PRO0138; MATRIXIN.  
DR SMART; SMO0120; HX; 4.  
DR SMART; SMO0235; ZnMc; 1.  
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC PROTEASE; 1.  
KW Calcium-binding; Collagen degradation; Extracellular matrix;  
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
KW Zymogen.  
FT SIGNAL 1 17 Probable.  
FT PROPEP 18 99 Activation peptide.  
FT CHAIN 100 477 Stromelysin-1.  
FT DOMAIN 287 477 Hemopexin-like.  
FT SITE 92 92 Cysteine switch (Potential).  
FT METAL 124 124 Calcium 1 (By similarity).  
FT METAL 158 158 Calcium 2 (By similarity).  
FT METAL 168 168 Zinc 1 (By similarity).  
FT METAL 170 170 Zinc 1 (By similarity).  
FT METAL 175 175 Calcium 3 (By similarity).  
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By  
similarity).  
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By  
similarity).  
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By  
similarity).  
FT METAL 183 183 Zinc 1 (By similarity).  
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By  
similarity).  
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By  
similarity).  
FT METAL 194 194 Calcium 2 (By similarity).  
FT METAL 196 196 Zinc 1 (By similarity).  
FT METAL 198 198 Calcium 3 (By similarity).  
FT METAL 199 199 Calcium 1 (By similarity).  
FT METAL 201 201 Calcium 1 and 3 (By similarity).  
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).  
FT ACT SITE 219 219 By similarity.  
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).  
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).  
FT METAL 297 297 Calcium 4 (via carbonyl oxygen) (By  
similarity).  
FT METAL 389 389 Calcium 4 (via carbonyl oxygen) (By  
similarity).  
FT METAL 438 438 Calcium 4 (via carbonyl oxygen) (By  
similarity).  
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).  
FT DISULFID 290 477 By similarity.  
FT CONFLICT 468 468 I -> T (in Ref. 3).  
SQ SEQUENCE 477 AA; 53845 MW; 9C15594F45262D37 CRC64;  
  
Query Match 51.6%; Score 133; DB 1; Length 477;  
Best Local Similarity 58.1%; Pred. No. 2.4e-09;  
Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00138; MATRILIXIN.  
 DR SMART; SMC0120; HX; 4.  
 DR SMART; SMC0235; ZNMC; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 479 AA; 54104 MW; 1FA89D6CF8FE5841 CRC64;

Query Match 51.68; Score 133; DB 2; Length 479;  
 Best Local Similarity 58.1%; Pred. No. 2.4e-09;  
 Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKW 43  
 Db 69 MQKFLGLEMTGKLDSTNMLMHPKRCGVPDVGGSTFFGSPKW 111

Search completed: November 15, 2004, 14:06:37  
 Job time : 45.3846 secs

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTFEGDLKW 43  
 Db 67 MQKFLGLEMTGKLDSTNMLMHPKRCGVPDVGGSTFFGSPKW 109

## RESULT 15

Q922W6 PRELIMINARY; PRT; 479 AA.  
 AC Q922W6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Matrix metalloproteinase 3.  
 GN Name=Mmp3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy.  
 RX MEDLINE=22368257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy.  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Brathwaite M., Waeltz P., Nagaraja R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006725; AAH06725.1; -  
 DR EMBL; AY211543; AAO37583.1; -  
 DR HSSP; P08254; IG05.  
 DR MGD; MGI:97010; Mmp3.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001843; Pept\_M10A\_M10C.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGSD\_like.  
 DR Pfam; PF02051; Fragilysin; 1.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.

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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 49.5 Seconds  
(without alignments)  
391.341 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFGKLVKTKPDAETLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17032 Human mat
4	292	100.0	454	7	ADL16002 G-coupled
5	292	100.0	454	7	ADL16004 G-coupled
6	292	100.0	454	7	ADL16008 G-coupled
7	292	100.0	454	7	ADL16006 G-coupled
8	292	100.0	454	8	ADL93945 Human G-c
9	292	100.0	454	8	ADL93943 Human G-c
10	292	100.0	455	8	ADL93941 Human G-c
11	292	100.0	463	4	AAB84606 Amino aci
12	292	100.0	469	4	AAE10415 Human mat
13	292	100.0	469	6	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU56596 Lung canc
18	292	100.0	469	6	ABU56597 Lung canc
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ADB79176 Matrix me
22	292	100.0	469	7	ADB34550 Human ski
23	292	100.0	469	7	ADL16000 G-coupled
24	292	100.0	469	7	ADL16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

26	292	100.0	469	7	ADN38694	Adn38694	Cancer/an
27	292	100.0	469	7	ADN38696	Adn38696	Cancer/an
28	292	100.0	469	7	ADN39850	Adn39850	Cancer/an
29	292	100.0	469	7	ADN95538	Adn95538	Human BEC
30	292	100.0	469	8	ADL93949	Adl93949	Human G-c
31	292	100.0	469	8	ADL93939	Adl93939	Human G-c
32	292	100.0	470	8	ADN07695	Adn07695	Human mat
33	292	100.0	490	7	ADL07892	Adl07892	Novel pro
34	292	100.0	496	4	AAG75509	Agg75509	Human col
35	286	97.9	457	1	AAP93628	Ap93628	Sequence
36	286	97.9	469	1	RAP70611	Rap70611	Sequence
37	286	97.9	469	8	ADQ18359	Adq18359	Human sof
38	292	97.6	454	8	ADL93947	Adl93947	Human G-c
39	214	73.3	55	6	ABP97132	Abp97132	Human mat
40	214	73.3	55	6	ABG76318	Abg76318	Human mat
41	214	73.3	55	8	ADQ17093	Adq17093	Human mat
42	214	73.3	444	4	RAG65357	Rag65357	Human MMP
43	214	73.3	467	4	RAB84610	Rab84610	Amino aci
44	214	73.3	467	4	AAE10416	Aae10416	Human mat
45	214	73.3	467	4	AAG65358	Agg65358	Human neu

#### ALIGNMENTS

RESULT 1

ABP97131

ID ABP97131 standard; peptide: 54 AA.

XX AC ABP97131;

XX DT 24-JUN-2003 (first entry)

XX DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;

XX KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;

XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;

XX KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;

XX KW dermatological; metastatic; non-metastatic; vascularised; heart disease;

XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;

XX KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX PN WO2003018748-A2.

XX PD 06-MAR-2003.

XX PF 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Weart IF;

XX DR WPI; 2003-381408/36.

XX PT Anti-angiogenic composition comprising peptide inhibitor of matrix

XX PT metalloproteinase, useful for decreasing the expression of vascular

XX PT endothelial growth factor and treating cancers and tissue injuries.

XX PS Claim 17; Page 16; 103pp; English.

XX CC The present invention describes an anti-angiogenic composition (I) for

XX CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)

XX CC comprises an effective amount of a peptide inhibitor of matrix

XX CC metalloproteinase (MMP), where the peptide can inhibit the expression of

XX CC VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective,

XX CC antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (I) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54  
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54

RESULT 2  
 ABG76317  
 ID ABG76317 standard; protein; 54 AA.

AC ABG76317;

DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #9.

XX Human; peptide inhibitor; matrix metalloproteinase-1; MMP-1;  
 XX cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026195.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix

XX metalloproteinases, e.g. matrix metalloproteinase-2, useful for

XX stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases  
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have  
 CC peptide sequences related to the cleavage regions of the proenzyme forms  
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular  
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin  
 CC development, treating wounds, preventing scarring, improving skin tone,  
 CC reducing wrinkling and for simulating the development of smooth, healthy  
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing  
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54  
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54

RESULT 3

ADQ17092

ID ADQ17092 standard; peptide; 54 AA.

XX ADQ17092;

XX 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-1 (MMP1) cleavage region peptide.

XX Fibronection; healthy skin; wrinkle; wound; vulnerary; dermatological;  
 XX human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds  
 XX comprises peptide having sequence related to matrix metalloproteinase  
 XX proenzyme.

XX Example 1; SEQ ID NO 9; 60pp; English.

XX The present invention provides peptides and compositions containing such  
 CC peptides that are useful as agents to maintain healthy skin and to  
 CC promote the condition of the skin. The invention is useful for increasing  
 CC the amount of fibronectin in tissue. The invention is also useful for  
 CC encouraging the maintenance and development of healthy skin, preventing  
 CC and treating wrinkles and for treating wounds. The invention acts as  
 CC vulnerary and dermatological agents. The present sequence is human matrix  
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in  
 CC the exemplification of the invention.

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54  
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQHTLTYYRIEN 54

RESULT 4

ADE16002

ID ADE16002 standard; protein; 454 AA.

XX ADE16002;

XX 29-JAN-2004 (first entry)

DE G-coupled protein receptor related polypeptide, SEQ ID No 32.  
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
XX preventive medicine; pharmacogenomics; human.  
XX Homo sapiens.  
XX WO200283841-A2.  
XX 24-OCT-2002.  
XX 03-APR-2002; 2002WO-US010713.  
XX 03-APR-2001; 2001US-0281136P.  
XX 05-APR-2001; 2001US-0281863P.  
XX 05-APR-2001; 2001US-0281906P.  
XX 10-APR-2001; 2001US-0282934P.  
XX 13-APR-2001; 2001US-0283657P.  
XX 13-APR-2001; 2001US-0283678P.  
XX 13-APR-2001; 2001US-0283687P.  
XX 13-APR-2001; 2001US-0283710P.  
XX 17-APR-2001; 2001US-0284234P.  
XX 19-APR-2001; 2001US-0285325P.  
XX 20-APR-2001; 2001US-0285609P.  
XX 23-APR-2001; 2001US-0285748P.  
XX 23-APR-2001; 2001US-0285890P.  
XX 24-APR-2001; 2001US-0286068P.  
XX 27-APR-2001; 2001US-0287213P.  
XX 30-MAY-2001; 2001US-0288509P.  
XX 31-MAY-2001; 2001US-0294495P.  
XX 31-MAY-2001; 2001US-0294801P.  
XX 31-JUL-2001; 2001US-0309216P.  
XX 25-SEP-2001; 2001US-0324775P.  
XX 28-NOV-2001; 2001US-0333900P.  
XX 02-APR-2002; 2002US-00115479.  
(CURA-) CURAGEN CORP.  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Gasman SJ, Boldog FL;  
PI Voss EZ, Vernet CM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX WPI: 2003-067574/06.  
XX N-PSDB; ADE16001.  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX Claim 1; SEQ ID NO 32; 320pp; English.  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidaemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX Sequence 454 AA;  
XX

Query Match 100.0%; Score 292; DB 7; Length 454;  
Best Local Similarity 100.0%; Pred No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MQEFFFGLKVTGKPDATLKVKNQPRCGVPDVAQFVLTGEGNPRWEQTHLTYYRIEN 54  
Db 50 MQEFFFGLKVTGKPDATLKVKNQPRCGVPDVAQFVLTGEGNPRWEQTHLTYYRIEN 103

RESULT 5  
ID ADE16004 standard; protein; 454 AA.  
XX ADE16004;  
XX 29-JAN-2004 (first entry)  
XX G-coupled protein receptor related polypeptide, SEQ ID No 34.  
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
XX preventive medicine; pharmacogenomics; human.  
XX Homo sapiens.  
XX WO200283841-A2.  
XX 24-OCT-2002.  
XX 03-APR-2002; 2002WO-US010713.  
XX 03-APR-2001; 2001US-0281136P.  
XX 05-APR-2001; 2001US-0281863P.  
XX 05-APR-2001; 2001US-0281906P.  
XX 10-APR-2001; 2001US-0282934P.  
XX 13-APR-2001; 2001US-0283657P.  
XX 13-APR-2001; 2001US-0283678P.  
XX 13-APR-2001; 2001US-0283687P.  
XX 13-APR-2001; 2001US-0283710P.  
XX 17-APR-2001; 2001US-0284234P.  
XX 19-APR-2001; 2001US-0285325P.  
XX 20-APR-2001; 2001US-0285609P.  
XX 23-APR-2001; 2001US-0285748P.  
XX 23-APR-2001; 2001US-0285890P.  
XX 24-APR-2001; 2001US-0286068P.  
XX 27-APR-2001; 2001US-0287213P.  
XX 30-MAY-2001; 2001US-0288509P.  
XX 31-MAY-2001; 2001US-0294495P.  
XX 31-MAY-2001; 2001US-0294801P.  
XX 31-JUL-2001; 2001US-0309216P.  
XX 25-SEP-2001; 2001US-0324775P.  
XX 28-NOV-2001; 2001US-0333900P.  
XX 02-APR-2002; 2002US-00115479.

PA (CURA-) CURAGEN CORP.  
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
 XX WPI: 2003-067574/06.  
 DR N-PSDB; ADE16003.  
 XX New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 PT Alzheimer's disease, infections.  
 XX Claim 1; SEQ ID NO 34; 320pp; English.  
 PS The invention relates to a novel isolated G-coupled protein receptor  
 XX related polypeptides. The novel polypeptide comprises any of the 22 fully  
 CC defined sequences of 87-1780 amino acids, given in the specification;  
 CC their mature forms; and possible variants. The novel polypeptides have  
 CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOVX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.  
 XX Sequence 454 AA;  
 SQ

Query Match 100.0%; Score 292; DB 7; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 2e-31;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MOEFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNRWEOHTLTYRIEN 54  
 DB 50 MQEFFFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNRWEOHTLTYRIEN 103

RESULT 6  
 ADE16008  
 ID ADE16008 standard; protein; 454 AA.  
 XX ADE16008;  
 AC ADE16008;  
 XX 29-JAN-2004 (first entry)  
 DT G-coupled protein receptor related polypeptide, SEQ ID NO 38.  
 DE G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
 KW virucide; fungicide; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

preventive medicine; pharmacogenomics; human.  
 Homo sapiens.  
 WO200283841-A2.  
 24-OCT-2002.  
 03-APR-2002; 2002WO-US010713.  
 03-APR-2001; 2001US-0281136P.  
 05-APR-2001; 2001US-0281863P.  
 05-APR-2001; 2001US-0281906P.  
 10-APR-2001; 2001US-0282934P.  
 13-APR-2001; 2001US-0283657P.  
 13-APR-2001; 2001US-0283678P.  
 13-APR-2001; 2001US-0283687P.  
 13-APR-2001; 2001US-0283710P.  
 17-APR-2001; 2001US-0284234P.  
 19-APR-2001; 2001US-0285325P.  
 20-APR-2001; 2001US-0285609P.  
 23-APR-2001; 2001US-0285748P.  
 23-APR-2001; 2001US-0285890P.  
 24-APR-2001; 2001US-0286068P.  
 27-APR-2001; 2001US-0287213P.  
 03-MAY-2001; 2001US-0288509P.  
 30-MAY-2001; 2001US-0294495P.  
 31-MAY-2001; 2001US-0294801P.  
 31-JUL-2001; 2001US-0309216P.  
 25-SEP-2001; 2001US-0324775P.  
 28-NOV-2001; 2001US-0333900P.  
 02-APR-2002; 2002US-00115479.  
 (CURA-) CURAGEN CORP.  
 Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
 Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
 Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
 WPI: 2003-067574/06.  
 N-PSDB; ADE16007.  
 New isolated NOVX polypeptides and polynucleotides, useful for  
 preventing, diagnosing or treating NOVX-associated disorders e.g.  
 diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 Alzheimer's disease, infections.  
 Claim 1; SEQ ID NO 38; 320pp; English.  
 The invention relates to a novel isolated G-coupled protein receptor  
 related polypeptides. The novel polypeptide comprises any of the 22 fully  
 defined sequences of 87-1780 amino acids, given in the specification;  
 their mature forms; and possible variants. The novel polypeptides have  
 the following activities: antidiabetic, anorectic, antibacterial,  
 virucide, fungicide, cytostatic, nootropic, neuroprotective,  
 antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
 receptor related polypeptides are useful in a method of treating or  
 preventing in a human, a pathology associated with the G-coupled protein  
 receptor related polypeptides. The polypeptides are useful in the  
 manufacture of a medicament for treating a syndrome associated with a  
 human disease, preferably a NOVX-associated disorder. The novel  
 polypeptides are useful for treating, preventing or diagnosing diseases,  
 such as metabolic disorders, diabetes, obesity, infectious diseases,  
 anorexia, cancer-associated diseases, neurodegenerative disorders,  
 Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 disorders, and various dyslipidaemias, metabolic disturbances associated  
 with obesity, metabolic X syndrome and wasting disorders associated with  
 chronic diseases and various cancers. The nucleic acids and polypeptides  
 may also be used as targets for the identification of small molecules  
 that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 therapy, in generation of antibodies that bind immunospecifically to NOVX  
 substances for use in therapeutic or diagnostic methods. The nucleic  
 acids are further used as hybridization probes, in chromosome mapping,  
 tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 represents one of the novel G-coupled protein receptor related  
 polypeptides of the invention.



CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFGKLVTKGKPDATLKVWKQRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
DB 50 MQEFGKLVTKGKPDATLKVWKQRCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 7  
AD216006  
ID ADE16006 standard; protein; 454 AA.

XX AC ADE16006;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE G-coupled protein receptor related polypeptide, SEQ ID No 36.  
XX  
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
KW preventive medicine; pharmacogenomics; human.

XX OS Homo sapiens.  
XX  
XX WO200293841-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010713.  
XX  
XX 03-APR-2001; 2001US-0281136P.  
XX 05-APR-2001; 2001US-0281863P.  
XX 05-APR-2001; 2001US-0281906P.  
XX 10-APR-2001; 2001US-0282934P.  
XX 13-APR-2001; 2001US-0283657P.  
XX 13-APR-2001; 2001US-0283678P.  
XX 13-APR-2001; 2001US-0283687P.  
XX 13-APR-2001; 2001US-0283710P.  
XX 17-APR-2001; 2001US-0284234P.  
XX 19-APR-2001; 2001US-0285325P.  
XX 20-APR-2001; 2001US-0285609P.  
XX 23-APR-2001; 2001US-0285748P.  
XX 23-APR-2001; 2001US-0285890P.  
XX 24-APR-2001; 2001US-0286068P.  
XX 27-APR-2001; 2001US-0287213P.  
XX 03-MAY-2001; 2001US-0288509P.  
XX 30-MAY-2001; 2001US-0294495P.  
XX 31-MAY-2001; 2001US-0294801P.  
XX 31-JUL-2001; 2001US-0309216P.  
XX 28-SEP-2001; 2001US-0324775P.  
XX 28-NOV-2001; 2001US-0333900P.  
XX 02-APR-2002; 2002US-00115479.

(CURA-) CURAGEN CORP.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
XX Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
XX Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
XX Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
XX Shimkets RA, Taupier RJ, Edinger SR, Mazur A;

XX WPI; 2003-067574/06.  
DR N-PSDB; ADE16005.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX

PS Claim 1; SEQ ID NO 36; 320pp; English.  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprises any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.

XX SQ Sequence 454 AA;  
Query Match 100.0%; Score 292; DB 7; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPDATLKVWKQRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
DB 50 MQEFGKLVTKGKPDATLKVWKQRCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 8  
ADL93945  
ID ADL93945 standard; protein; 454 AA.  
XX AC ADL93945;  
XX  
XX 20-MAY-2004 (first entry)  
XX  
DE Human G-coupled protein receptor-related protein #18.

XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;  
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;  
KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;  
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;  
KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;  
KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;  
KW Crohn's disease; G-coupled protein receptor; metabolic disorder;  
KW neurodegenerative disorder; receptor.



Query Match 100.0%; Score 292; DB 8; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-31;

Query Match 100.0%; Score 292; DB 8; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-31;

PA	(MACB/)	MACDOUGALL J R.
PA	(RAST/)	RASTELLI L.
PA	(ANDE/)	ANDERSON D W.
PA	(ZHON/)	ZHONG M.
PA	(MEZE/)	MEZES P S.
PA	(FURT/)	FURTAK K.
PA	(PATT/)	PATTURAJAN M.
PA	(BURG/)	BURGESS C E.
PA	(MALY/)	MALYANKAR U M.
PA	(SHIM/)	SHINKETS R A.
PA	(TAUP/)	TAUPIER R J.
PA	(EDIN/)	EDINGER S.
PA	(MAZU/)	MAZUR A.

Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI  
Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI  
Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;  
PI  
Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI  
Shinkets RA, Taupier RJ, Edinger S, Nazur A;  
PI

WPI; 2004-224146/21.  
N-PSDB: ADL93940.

New G-coupled protein-receptor related polypeptides, for preventing PT  
treating or ameliorating, e.g. acquired immunodeficiency syndrome, PT  
bronchial asthma, Crohn's disease, prostate cancer, hemophilia, PT  
scleroderma or obesity. PT

Sequence 455 AA:

Query Match 100.0%; Score 292; DB 8; Length 455;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 MQEFFGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
50 MQEFFGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 11  
AAB84606  
IID AAB84606 standard; protein; 469 AA.  
XX  
AC AAB84606;

KW KW KW XX OS XX PN XX PD XX PF XX PR XX PA PA XX PI XX DR DR

Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth factor.

Sequence 469 AA;

Query Match 100.0%; Score 292; DB 4; Length 469;  
Best Local Similarity 100.0%; Pred. No. 2.1e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 12  
AAE10415  
ID AAE10415 standard; protein: 469 AA.



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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX
XX WPI: 2003-354600/33.
XX N-PSDB; ACC72663.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 735; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR59521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX CC atherosclerosis and endometriosis. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 469 AA;
XX
XX Query Match 100.0%; Score 292; DB 6; Length 469;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQEFFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
XX Db 67 MQEFFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
XX
XX RESULT 15
XX ABR58542
XX ID ABR58542 standard; protein; 469 AA.
XX AC ABR58542;
XX
XX DT 09-JUL-2003 (first entry)
XX
XX DE Human cancer related protein SEQ ID NO:199.
XX
XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW heart disease; atherosclerosis; endometriosis.
XX
XX OS Homo sapiens.
XX
XX PN WO2003025138-A2.
XX
XX PD 27-MAR-2003.
XX
XX PF 17-SEP-2002; 2002WO-US029560.
XX
XX PR 17-SEP-2001; 2001US-0323469P.
XX
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PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
XX Zlotnik A;
XX
XX WPI: 2003-354600/33.
XX N-PSDB; ACC72662.
XX
XX New genes that are up-regulated or down-regulated in cancers, useful as
XX PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX PT therapeutic targets for screening drugs for treating these diseases.
XX
XX Claim 12; Page 735; 767pp; English.
XX
XX The present invention describes an isolated nucleic acid molecule, which
XX CC comprises the sequence of any of the genes that are up-regulated or down-
XX CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
XX CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
XX CC related gene nucleotide sequences which encode the proteins given in
XX CC ABR59521 to ABR58709. Also described: (1) determining the presence or
XX CC absence of a pathological cell in a patient; (2) an expression vector
XX CC comprising a nucleic acid molecule described above; (3) a host cell
XX CC comprising the vector; (4) an isolated polypeptide, which is encoded by
XX CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
XX CC of (4); (6) specifically targeting a compound to a pathological cell in a
XX CC patient by administering to the patient the antibody above; and (7) a
XX CC drug screening assay. The nucleic acid is useful as diagnostic markers or
XX CC therapeutic targets. In particular, the nucleic acid is useful for
XX CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
XX CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
XX CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
XX CC atherosclerosis and endometriosis. The nucleic acid is also useful in
XX CC drug screening, particularly for identifying agents for treating these
XX CC pathologies
XX SQ Sequence 469 AA;
XX
XX Query Match 100.0%; Score 292; DB 6; Length 469;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQEFFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
XX Db 67 MQEFFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
XX
XX Search completed: November 15, 2004, 14:04:09
XX Job time : 51.5 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 14.5385 Seconds  
(without alignments)  
246.324 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MGEFFGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_5/protdata/1/iaa/5A COMB.pep:\*  
2: /cgn2\_5/protdata/1/iaa/5B COMB.pep:\*  
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4: /cgn2\_5/protdata/1/iaa/6B COMB.pep:\*  
5: /cgn2\_5/protdata/1/iaa/PCITUS COMB.pep:\*  
6: /cgn2\_5/protdata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	3	US-08-704-711A-16
2	292	100.0	469	3	US-08-448-489-12
3	292	100.0	469	3	US-09-521-220-16
4	292	100.0	469	3	US-09-391-104-23
5	214	73.3	444	1	US-09-178-002-2
6	214	73.3	466	3	US-08-704-711A-17
7	214	73.3	466	1	US-09-521-220-17
8	214	73.3	467	3	US-09-178-002-4
9	214	73.3	467	3	US-09-391-104-24
10	214	73.3	468	3	US-08-448-489-13
11	189	64.7	476	3	US-08-704-711A-21
12	189	64.7	476	3	US-08-448-489-14
13	189	64.7	476	3	US-09-521-220-21
14	189	64.7	476	3	US-09-391-104-22
15	189	64.7	477	3	US-08-704-711A-20
16	189	64.7	477	3	US-08-448-489-15
17	189	64.7	477	3	US-08-281-313-1
18	189	64.7	477	3	US-09-521-220-20
19	189	64.7	477	3	US-09-391-104-21
20	163	55.8	471	3	US-09-391-104-25
21	163	55.8	513	4	US-10-140-002-192
22	163	55.8	513	4	US-09-862-631-4
23	159	54.5	470	3	US-08-068-392-2
24	159	54.5	470	3	US-08-396-988-2
25	159	54.5	470	3	US-09-391-104-26
26	134	52.7	471	4	US-08-394-689C-1
27	151	51.7	264	3	US-09-009-156-6

28 151 51.7 264 3 US-09-372-154-6 Sequence 6, Appli  
29 151 51.7 267 3 US-08-448-489-18 Sequence 18, Appl  
30 151 51.7 267 3 US-08-391-104-27 Sequence 27, Appl  
31 151 51.7 271 3 US-08-896-062-2 Sequence 2, Appl  
32 150 51.4 135 4 US-09-513-999C-4163 Sequence 21, Appl  
33 147 50.3 471 4 US-08-994-689C-21 Sequence 21, Appl  
34 144 49.3 462 3 US-08-068-392-3 Sequence 3, Appl  
35 144 49.3 462 3 US-08-396-988-3 Sequence 3, Appl  
36 144 49.3 631 3 US-08-448-489-17 Sequence 17, Appl  
37 144 49.3 660 3 US-08-704-711A-18 Sequence 18, Appl  
38 144 49.3 660 3 US-09-521-220-18 Sequence 18, Appl  
39 144 49.3 660 3 US-09-391-104-19 Sequence 19, Appl  
40 144 49.3 660 4 US-09-917-254-89 Sequence 89, Appl  
41 136.5 46.7 604 3 US-09-391-104-30 Sequence 30, Appl  
42 136.5 46.7 607 3 US-09-000-041A-2 Sequence 2, Appl  
43 136.5 46.7 607 3 US-09-211-704A-10 Sequence 10, Appl  
44 136.5 46.7 607 4 US-09-734-002-2 Sequence 2, Appl  
45 134.5 46.1 582 3 US-08-704-711A-2 Sequence 2, Appl

#### ALIGNMENTS

RESULT 1  
US-08-704-711A-16  
; Sequence 16, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/704,711A  
; FILING DATE: 20-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DE95/00357  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 469 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-704-711A-16

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

## RESULT 2

US-08-448-489-12  
Sequence 12, Application US/08448489  
Patent No. 6184022  
GENERAL INFORMATION:  
APPLICANT: SEIKI, Motoharu  
APPLICANT: SATO, Hiroshi  
APPLICANT: SHINAGAWA, Akira  
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
FILE REFERENCE: 55-290P  
CURRENT APPLICATION NUMBER: US/08/448,489  
CURRENT FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Known Member of  
OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-12

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

## RESULT 3

US-09-521-220-16  
Sequence 16, Application US/09521220  
Patent No. 639348  
GENERAL INFORMATION:  
APPLICANT: WILL, Horst  
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
METALLOPROTEASES, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/521,220  
FILING DATE: 08-Mar-2000  
CLASSIFICATION: <Unknown>  
21-OCT-1994  
17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/704,711  
FILING DATE: <Unknown>

APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 469 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-521-220-16

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

## RESULT 4

US-09-391-104-23  
Sequence 23, Application US/09391104  
Patent No. 639371  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Falguto, Michael T.  
APPLICANT: Magnuson, Scott R.  
APPLICANT: Morgan, Douglas W.  
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
TITLE OF INVENTION: OF USING SAME  
FILE REFERENCE: 6073.US.P1  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07  
PRIOR APPLICATION NUMBER: US 08/814,394  
PRIOR FILING DATE: 1997-03-11  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-391-104-23

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

## RESULT 5

US-09-178-002-2  
Sequence 2, Application US/09178002  
Patent No. H001973  
GENERAL INFORMATION:  
APPLICANT: Hu, Shou-Ih  
TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
FILE REFERENCE: CGC 2048  
CURRENT APPLICATION NUMBER: US/09/178,002



1 MOEFFGLKVTGKPDATLTKVMKPRCGVDPVQAQFVLTEGPNRWEQTHLTYRIEN 54  
 Db 66 MORFFGLNVTGKPNSETLDMMKKPRCGVDPGSGFMLTGPNKWRINLTYRIEN 119

RESULT 7  
 US-09-521-220-17  
 ; Sequence 17, Application US/09521220  
 ; Patent No. 6398348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILLI, Horst  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; METALLOPROTEASES, THEIR PRODUCTION AND USE  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; FILING APPLICATION NUMBER: US/09/521.220  
 ; FILING DATE: 08-Mar-2000  
 ; CLASSIFICATION: <Unknown>  
 ; 21-OCT-1994  
 ; 17-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/704,711  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: DE 4438838.1  
 ; FILING DATE: 21-OCT-1994  
 ; APPLICATION NUMBER: DE 4409663.1  
 ; FILING DATE: 17-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GRANADOS, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 26083/124  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 466 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
 ; US-09-521-220-17  
 ;  
 ; Query Match 73.3%; Score 214; DB 3; Length 466;  
 ; Best Local Similarity 70.4%; Pred. No. 1.3e-20;  
 ; Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0

1 MOEFFGLKVTGKPDATLTKVMKPRCGVDPVQAQFVLTEGPNRWEQTHLTYRIEN 54  
 Db 66 MORFFGLNVTGKPNSETLDMMKKPRCGVDPGSGFMLTGPNKWRINLTYRIEN 119

RESULT 8  
 US-09-178-002-4  
 ; Sequence 4, Application US/09178002  
 ; Patent No. H001973  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hu, Shou-Ih

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; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

Query Match      73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFGKLVGTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 MQRFFGLNVTGKNEETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRIN 119

RESULT 9
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match      73.3%; Score 214; DB 3; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFGKLVGTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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Db 66 MQRFFGLNVTGKNEETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRIN 119

RESULT 10
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

Query Match      64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVGTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 MQKFLGLEVTGKLDITLLEWKRKPCGVPDVGHFSSFFGMPKWKXKTHLYRIIN 119

; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match      73.3%; Score 214; DB 3; Length 468;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFGKLVGTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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Db 66 MQRFFGLNVTGKNEETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRIN 119

RESULT 11
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-21

Query Match      64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVGTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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Db 66 MQKFLGLEVTGKLDITLLEWKRKPCGVPDVGHFSSFFGMPKWKXKTHLYRIIN 119
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RESULT 12

US-08-448-489-14

Sequence 14, Application US/08448489

Patent No. 6184022

GENERAL INFORMATION:

APPLICANT: SEIKI, Motoharu

APPLICANT: SATO, Hiroshi

APPLICANT: SHINAGAWA, Akira

TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR

FILE REFERENCE: 55-290P

CURRENT APPLICATION NUMBER: US/08/448,489

CURRENT FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

LENGTH: 476

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Known Member of

OTHER INFORMATION: Matrix Metalloproteinase Family

US-08-448-489-14

Query Match 64.7%; Score 189; DB 3; Length 476;

Best Local Similarity 63.08; Pred. No. 3,2e-17;

Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQSFFGLKVTGKPAETLKNVKPRCGVPDVAQVLTGEGNPRWQTHLTYRIEN 54

Db 66 MQKFLGLEVTGKLDTDLEVNKRKPCGVDPYGHFSSFFGMEKWKXKTHLTYRIVN 119

RESULT 13

US-09-521-220-21

Sequence 21, Application US/09521220

Patent No. 6399348

GENERAL INFORMATION:

APPLICANT: WILL, Horst

HINZMANN, Bernd

TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX

METALLOPROTEASES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/521,220

FILING DATE: 08-Mar-2000

CLASSIFICATION: <unknown>

21-OCT-1994

17-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,711

FILING DATE: <unknown>

APPLICATION NUMBER: DE 4438838.1

FILING DATE: 21-OCT-1994

APPLICATION NUMBER: DE 4409663.1

FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: GRANADOS, Patricia D.

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26083/124

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-20

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Query Match      64.7%; Score 189; DB 3; Length 477;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MQEFTGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWQTHLTYPRIEN 54
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Search completed: November 15, 2004, 14:08:07  
Job time : 14.5385 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 139.846 Seconds  
(without alignments)  
136.623 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFGKLVTKGPKDAETLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	54	14	US-10-219-329-9
2	292	100.0	54	14	US-10-153-185-9
3	292	100.0	54	14	US-10-219-561-9
4	292	100.0	54	16	US-10-032-376A-9
5	292	100.0	54	16	US-10-335-207-9
6	292	100.0	454	15	US-10-115-479-32
7	292	100.0	454	15	US-10-115-479-34
8	292	100.0	454	15	US-10-115-479-36
9	292	100.0	454	15	US-10-115-479-38
10	292	100.0	469	9	US-09-391-104-23
11	292	100.0	469	9	US-09-801-196-19
12	292	100.0	469	9	US-09-853-385-100
13	292	100.0	469	14	US-10-301-822-119

14	292	100.0	469	14	US-10-021-660-76	Sequence 76, Appl
15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	14	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	14	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	14	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	14	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appl
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	470	16	US-10-447-315-1	Sequence 1, Appl
27	292	100.0	496	14	US-10-106-698-6283	Sequence 6283, Ap
28	292	100.0	496	14	US-10-219-329-10	Sequence 10, Appl
29	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
30	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
31	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
32	214	73.3	55	16	US-10-335-207-10	Sequence 10, Appl
33	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
34	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
35	214	73.3	467	10	US-09-759-130B-176	Sequence 176, App
36	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
37	214	73.3	467	16	US-10-741-790-176	Sequence 176, App
38	200.5	68.7	267	14	US-10-133-797-73	Sequence 73, Appl
39	191	65.4	173	15	US-10-115-479-48	Sequence 48, Appl
40	190.5	65.2	325	15	US-10-115-479-78	Sequence 78, Appl
41	189	64.7	54	14	US-10-219-329-5	Sequence 5, Appl
42	189	64.7	54	14	US-10-153-185-5	Sequence 5, Appl
43	189	64.7	54	14	US-10-219-561-5	Sequence 5, Appl
44	189	64.7	54	16	US-10-032-376A-5	Sequence 5, Appl
45	189	64.7	54	16	US-10-335-207-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-10-219-329-9  
; Sequence 9, Application US/10219329  
; Publication No. US20030096757A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Weart, Ilona f.  
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds  
; FILE REFERENCE: 1443.03SWOI  
; CURRENT APPLICATION NUMBER: US/10/219,329  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-329-9

Query Match 100.0%; Score 292; DB 14; Length 54;  
Best Local Similarity 100.0%; Pred. No. 4.4e-30;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQEFGKLVTKGPKDAETLKVKOPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
Db 1 MQEFGKLVTKGPKDAETLKVKOPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
RESULT 2  
US-10-153-185-9  
; Sequence 9, Application US/10153185  
; Publication No. US20030148959A1

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-9

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Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 3
US-10-219-561-9
; Sequence 9, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-032-376A-9
; Sequence 9, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
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; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-9

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Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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RESULT 5
US-10-335-207-9
; Sequence 9, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronection
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-9

Query Match      100.0%; Score 292; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 6
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
```

APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
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PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
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NUMBER OF SEQ ID NOS: 198  
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LENGTH: 454  
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US-10-115-479-32

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Best Local Similarity 100.0%; Pred. No. 5e-29;  
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RESULT 7  
US-10-115-479-34  
Sequence 34, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
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PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 34  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-34

Query Match 100.0%; Score 292; DB 15; Length 454;  
Best Local Similarity 100.0%; Pred. No. 5e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFFGLKVTGKPDASTLKVWKQRCGVPDVAQFVLTGEGNPRWEQHTLYRIEN 54  
DB 50 MQEFFGLKVTGKPDASTLKVWKQRCGVPDVAQFVLTGEGNPRWEQHTLYRIEN 103

RESULT 8  
US-10-115-479-36  
Sequence 36, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 36  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;  
Best Local Similarity 100.0%; Pred. No. 5e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGNPRWEQTHLYTYRIEN 54  
DB 50 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGNPRWEQTHLYTYRIEN 103

RESULT 9  
US-10-115-479-38  
Sequence 38, Application US/10/115479  
Publication No. US2004006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glenda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 38  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;  
Best Local Similarity 100.0%; Pred. No. 5e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGNPRWEQTHLYTYRIEN 54  
DB 50 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGNPRWEQTHLYTYRIEN 103

RESULT 10  
US-09-391-104-23  
Sequence 23, Application US/09391104  
Publication No. US20020031817A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Palduto, Michael T.  
APPLICANT: Magnuson, Scott R.  
APPLICANT: Morgan, Douglas W.  
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
FILE REFERENCE: 6073.US.P1  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07  
PRIOR APPLICATION NUMBER: US 08/814,394  
PRIOR FILING DATE: 1997-03-11  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-391-104-23  
Query Match 100.0%; Score 292; DB 9; Length 469;



Best Local Similarity 100.0%; Pred. No. 5.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 11

US-09-801-196-19  
; Sequence 19, Application US/09801196  
; Patent No. US20020037827A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Kai  
; APPLICANT: Smith, Ryan  
; APPLICANT: Pajardo, Mark  
; APPLICANT: Moss, Patrick  
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)  
; FILE REFERENCE: 240083.509  
; CURRENT APPLICATION NUMBER: US/09/801,196  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-801-196-19

Query Match 100.0%; Score 292; DB 9; Length 469;  
Best Local Similarity 100.0%; Pred. No. 5.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 12

US-09-853-386-100  
; Sequence 100, Application US/09853386  
; Patent No. US20020049151A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Evelyn  
; APPLICANT: Bresnahan, Barry  
; APPLICANT: Conneely, Orla  
; APPLICANT: Fitzgerald, Oliver  
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR  
; FILE REFERENCE: P01972US1  
; CURRENT APPLICATION NUMBER: US/09/853,386  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203645  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-853-386-100

Query Match 100.0%; Score 292; DB 9; Length 469;  
Best Local Similarity 100.0%; Pred. No. 5.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 13

US-09-853-386-100

US-10-301-822-119  
; Sequence 119, Application US/10301822  
; Publication No. US20030148410A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Berger, Allison  
; APPLICANT: Guillemette, Tracy L.  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Thibodeau, Stephen N.  
; APPLICANT: Burgart, Lawrence J.  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MEM01-029P2RNM  
; CURRENT APPLICATION NUMBER: US/10/301,822  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/339,971  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/351,978  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/381,988  
; PRIOR FILING DATE: 2002-05-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-301-822-119

Query Match 100.0%; Score 292; DB 14; Length 469;  
Best Local Similarity 100.0%; Pred. No. 5.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54  
Db 67 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 120

RESULT 14

US-10-021-660-76  
; Sequence 76, Application US/10021660  
; Publication No. US20030152926A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: EOS Biotechnology, Inc.  
; TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,  
; FILE REFERENCE: Compositions and Methods of Screening for Angiogenesis  
; TITLE OF INVENTION: Modulators  
; FILE REFERENCE: C18501-000710US  
; CURRENT APPLICATION NUMBER: US/10/021,660  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US/09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/637,977  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-021-660-76

Query Match 100.0%; Score 292; DB 14; Length 469;  
Best Local Similarity 100.0%; Pred. No. 5.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDAAETLKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54

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Db      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 120
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RESULT 15
US-10-308-279-34
; Sequence 34, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-308-279-34

Query Match      100.0%; Score 292; DB 14; Length 469;
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Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 54
|||||
Db      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 120
|||||

Search completed: November 15, 2004, 14:22:34
Job time : 139.846 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.1154 Seconds  
(without alignments)  
428.852 Million cell updates/sec

Title: US-10-032-376A-9  
Perfect score: 292  
Sequence: 1 MQEFGGLKVTGKPAETLKV.....VLTEGNRWETHLTPIEN 54

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246014

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: Pir1:.\*  
2: Pir2:.\*  
3: Pir3:.\*  
4: Pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	468	1 KCRBI	interstitial colla
3	270	92.5	469	1 KCPGI	interstitial colla
4	234	80.1	469	1 KCB0I	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase (EC 3.4.11.1)
6	214	73.3	467	1 KCHUN	neutrophil collage
7	189	64.7	476	1 KCHUS2	stromelysin 2 (EC 3.4.21.2)
8	189	64.7	477	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
9	186	63.7	478	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
10	173	59.2	476	1 JCE505	stromelysin 2 (EC 3.4.21.2)
11	172	59.2	477	1 KCRSS1	stromelysin 1 (EC 3.4.21.2)
12	172	58.9	475	1 KCRTH	stromelysin 1 (EC 3.4.21.2)
13	172	58.9	483	2 JCS743	matrix metallopro
14	168	57.5	472	2 S23243	interstitial colla
15	167	57.2	476	1 KCRTS2	collagenase 3 (EC 3.4.21.2)
16	163	55.8	471	2 A53711	interstitial colla
17	162	55.5	466	2 A23685	interstitial colla
18	159	54.5	470	2 A43499	metalloproteinase
19	155	53.1	267	2 A57490	matrix metallopro
20	151	51.7	267	1 KCHUM	matrix metallopro
21	144	49.3	462	2 A42401	gelatinase A (EC 3.4.21.2)
22	144	49.3	660	1 A28153	gelatinase A (EC 3.4.21.2)
23	134.5	46.1	582	2 I38028	matrix metallopro
24	126.5	43.3	582	2 I84471	matrix metallopro
25	124	42.5	82	2 PW0052	pro-matrix metallo
26	118.5	40.6	582	2 I48673	matrix metallopro
27	111	38.0	364	2 E71433	probable metallopro
28	108	37.0	341	2 T51957	metalloproteinase
29	108	37.0	342	2 G84885	probable metallopro

## RESULT 1

## KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C:Species: Homo sapiens (man)  
C:Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004  
C:Accession: A37308, S22766; I57620; A00996; D29157; A44518; S06130; B60964; S10595; S51  
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St  
Cancer Res. 50, 5431-5437, 1990  
A:Title: Cloning and characterization of human tumor cell interstitial collagenase.  
A:Reference number: A37308; MUID:90352587; PMID:2167156  
A:Accession: A37308  
A:Molecule type: mRNA  
A:Residues: 1-469 <TEM>  
A:Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126  
R:Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.  
J. Clin. Invest. 79, 542-546, 1987  
A:Title: Molecular cloning of human synovial cell collagenase and selection of a single  
A:Reference number: S22766; MUID:87109799; PMID:3027129  
A:Accession: S22766  
A:Molecule type: DNA  
A:Residues: 1-63,65-70 <BRI>  
A:Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667  
R:Angel, P.; Baumann, I.; Stein, B.; Dellus, H.; Rahmsdorf, H.J.; Herrlich, P.  
Mol. Cell. Biol. 7, 2256-2266, 1987  
A:Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene:  
A:Reference number: I57620; MUID:87257941; PMID:3037355  
A:Accession: I57620  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-35 <RES>  
A:Cross-references: GB:M16567; NID:G180668; PIDN:AAA35699.1; PID:G180669  
R:Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.  
J. Biol. Chem. 261, 6600-6605, 1986  
A:Title: Human fibroblast collagenase. Complete primary structure and homology to an on  
A:Reference number: A00996; MUID:86196089; PMID:3009463  
A:Accession: A00996  
A:Molecule type: mRNA  
A:Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>  
A:Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665  
A:Note: part of this sequence was confirmed by protein sequencing of the proenzyme  
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris  
Biochem. J. 240, 913-916, 1986  
A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis.  
A:Reference number: A90336; MUID:87156645; PMID:3030290  
A:Accession: D29157  
A:Molecule type: mRNA  
A:Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>  
A:Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA28858.1; PID:G38267  
A:Note: parts of this sequence, including the amino end of the proenzyme and of the mat  
R:Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Brown, A.S.; Birkedal-Hansen, H.  
Biochemistry 27, 6751-6758, 1988

## ALIGNMENTS

30	106.5	36.5	305	2	T08836
31	103.5	35.4	579	2	T32428
32	103.5	35.4	598	2	T32166
33	100	34.2	521	2	T37252
34	92.5	31.7	587	2	S12805
35	92	31.5	508	2	JCS082
36	91	31.2	488	2	S13423
37	89.5	30.7	378	2	E96724
38	85.5	29.3	477	1	I51645
39	85.5	29.3	587	2	S41409
40	83	28.4	616	2	JC7776
41	82	28.1	492	2	A44399
42	80	27.4	377	2	T00643
43	79	27.1	491	2	JC6197
44	69.5	23.8	170	2	T17286
45	61	20.9	478	2	T32825

probable metallopro  
probable matrix me  
hypothetical prote  
probable matrix me  
envelysin (EC 3.4.  
matrix metalloprot  
stromelysin 3 (EC  
hypothetical prote  
stromelysin 3 (EC  
envelysin (EC 3.4.  
matrix metalloprot  
stromelysin 3 (EC  
zinc metalloprotei  
stromelysin 3 (EC  
hypothetical prote  
hypothetical prote

Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGPDATLTKMKQPCGVPDVAQFVLTEGNPWEQTHLYRIEN 54  
|||||  
DB 67 MQEFFGLKVTGPDATLTKMKQPCGVPDVAQFVLTEGNPWEQTHLYRIEN 120  
|||||

RESULT 2

KCRBI

N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A27500; B27500; I46694  
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.  
Biochemistry 26, 6156-6165, 1987  
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote  
A;Reference number: A27500; MUID:88077876; PMID:2825772  
A;Accession: A27500  
A;Molecule type: mRNA  
A;Residues: 1-468 <FIN>  
A;Cross-references: UNIPROT:PI3943; GB:M19240  
A;Accession: B27500  
A;Molecule type: DNA  
A;Residues: 1-391;399-468 <FT2>  
A;Cross-references: GB:M17820  
A;Note: the location of the intron between exons 7 and 8 is approximate  
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho  
Coll. Relat. Res. 6, 239-248, 1986  
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial  
A;Reference number: I46694; MUID:87029174; PMID:3021384  
A;Accession: I46694  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 449-468 <F13>  
A;Cross-references: GB:M25663; NID:G531211; PIDN:AAA31203.1; PID:G531212  
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th  
tion peptide by other proteinases.  
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C;Genetics:  
A;Introns: 34/3; 116/2; 166/1; 208/1; 299/2; 344/1; 398/1; 433/1  
C;Function:  
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
C;Superfamily: interstitial collagenase; hemoxin repeat homology; matrix metalloprotei  
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-468/Product: procollagenase #status predicted <PRO>  
F;19-98/Domain: activation peptide #status predicted <ACT>  
F;59-260/Domain: matrix metalloproteinase homology <MMP>  
F;89-96/Region: autoinhibitory  
F;99-468/Product: interstitial collagenase #status predicted <MAT>  
F;271-465/Domain: hemoxin repeat homology <PXN>  
F;31-172/221/227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;119-142/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;217-221/227/Binding site: zinc, catalytic (His) (active) #status predicted  
F;218/Active site: Glu #status predicted  
F;277-465/Disulfide bonds: #status predicted

Query Match 96.9%; Score 283; DB 1; Length 468;  
Best Local Similarity 96.3%; Pred. No. 3.6e-27;  
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGPDATLTKMKQPCGVPDVAQFVLTEGNPWEQTHLYRIEN 54  
|||||  
DB 66 MQEFFGLKVTGPDATLTKMKQPCGVPDVAQFVLTEGNPWEQTHLYRIEN 119  
|||||

RESULT 3

KCRGI

N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A27500; B27500; I46694  
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.  
Biochemistry 26, 6156-6165, 1987  
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote  
A;Reference number: A27500; MUID:88077876; PMID:2825772  
A;Accession: A27500  
A;Molecule type: mRNA  
A;Residues: 1-468 <FIN>  
A;Cross-references: UNIPROT:PI3943; GB:M19240  
A;Accession: B27500  
A;Molecule type: DNA  
A;Residues: 1-391;399-468 <FT2>  
A;Cross-references: GB:M17820  
A;Note: the location of the intron between exons 7 and 8 is approximate  
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho  
Coll. Relat. Res. 6, 239-248, 1986  
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial  
A;Reference number: I46694; MUID:87029174; PMID:3021384  
A;Accession: I46694  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 449-468 <F13>  
A;Cross-references: GB:M25663; NID:G531211; PIDN:AAA31203.1; PID:G531212  
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th  
tion peptide by other proteinases.  
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C;Genetics:  
A;Introns: 34/3; 116/2; 166/1; 208/1; 299/2; 344/1; 398/1; 433/1  
C;Function:  
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
C;Superfamily: interstitial collagenase; hemoxin repeat homology; matrix metalloprotei  
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-468/Product: procollagenase #status predicted <PRO>  
F;19-98/Domain: activation peptide #status predicted <ACT>  
F;59-260/Domain: matrix metalloproteinase homology <MMP>  
F;89-96/Region: autoinhibitory  
F;99-468/Product: interstitial collagenase #status predicted <MAT>  
F;271-465/Domain: hemoxin repeat homology <PXN>  
F;31-172/221/227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;119-142/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;217-221/227/Binding site: zinc, catalytic (His) (active) #status predicted  
F;218/Active site: Glu #status predicted  
F;277-465/Disulfide bonds: #status predicted

C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: S15986; S23597  
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.  
Matrix 11, 161-167, 1991  
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of  
A:Reference number: S15986; MUID:91333421; PMID:1651440  
A:Accession: S15986  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-469 <RIC>  
A:Cross-references: UNIPROT:P21692  
A:Note: Part of the sequence, including the amino end of the proenzyme, was confirmed by  
R:Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.  
Nucleic Acids Res. 18, 6703, 1990  
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.  
A:Reference number: S15597; MUID:91067477; PMID:2174547  
A:Accession: S15597  
A:Molecule type: mRNA  
A:Residues: 25-469 <CLA>  
A:Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269  
R:Li, J.; Brick, P.; Blow, D.M.  
submitted to the Brookhaven Protein Data Bank, April 1995  
A:Reference number: A65568; PDB:1FBL  
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466  
C:Comment: Procollagenase can be activated without removal of the activation peptide. S  
tion peptide by other proteinases.  
C:Function: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
A:Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-469/Product: procollagenase #status predicted <PRO>  
F:20-99/Domain: activation peptide #status experimental <ACT>  
F:60-261/Domain: matrix metalloproteinase homology <MMP>  
F:100-469/Product: interstitial collagenase #status predicted <MAT>  
F:272-466/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
F:219/Active site: Glu #status predicted  
F:219/Active site: Glu #status predicted  
F:278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;  
Best Local Similarity 90.7%; Pred. No. 1.5e-25;  
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54  
DB 67 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 4  
KCHOI  
Interstitial collagenase (EC 3.4.24.7) precursor - bovine  
N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: S14654; S20336; S14655  
R:Tamura, M.; Shimokawa, H.; Sasaki, S.  
submitted to the EMBL Data Library, March 1991  
A:Reference number: S14654  
A:Accession: S14654  
A:Molecule type: mRNA  
A:Residues: 1-469 <TAM>  
A:Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260  
R:Stuckey, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.  
Arch. Biochem. Biophys. 293, 370-376, 1992  
A:Title: Purification and characterization of bovine interstitial collagenase and tissue  
A:Reference number: S20336; MUID:92161820; PMID:1311165  
A:Accession: S20336

A:Molecule type: protein  
A:Residues: 19-21, 'pp', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125  
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th  
C:Comment: Procollagenase can be activated without removal of the activation peptide. S  
tion peptide by other proteinases.  
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of wh  
C:Function:  
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-469/Product: procollagenase #status predicted <PRO>  
F:19-99/Domain: activation peptide #status predicted <ACT>  
F:60-261/Domain: matrix metalloproteinase homology <MMP>  
F:90-97/Region: autoinhibitory  
F:100-469/Product: interstitial collagenase #status predicted <MAT>  
F:272-466/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F:219/Active site: Glu #status predicted  
F:278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;  
Best Local Similarity 81.5%; Pred. No. 4.2e-21;  
Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54  
DB 67 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 5  
151267  
collagenase (EC 3.4.24.-) - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: 151267  
R:Corruga, K.; Yomori, S.; Yoshizato, K.  
Int. J. Dev. Biol. 38, 345-350, 1994  
A:Title: Regionally and hormonally regulated expression of genes of collagen and collag  
A:Reference number: 151267; MUID:95071832; PMID:7981043  
A:Accession: 151267  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-384 <OOP>  
A:Cross-references: UNIPROT:Q11133; GB:S75623; NID:g913070; PIDN:AAB32661.1; PID:g91307  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F:53-231/Domain: matrix metalloproteinase homology <MMP>  
F:236-381/Domain: hemopexin repeat homology <PXN>  
F:81,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted  
F:190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;  
Best Local Similarity 79.6%; Pred. No. 6.9e-21;  
Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54  
DB 57 LKQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 109

RESULT 6  
KCHUN  
neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human  
N/Alternate names: matrix metalloproteinase 8  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A37073; A61175; A36230; S09680; S11026; S19576; S27225; S32527; S6  
R:Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev  
J. Biol. Chem. 265, 11421-11424, 1990

A;Title: Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.  
 A;Reference number: A37073; MUID:90307647; PMID:2164002  
 A;Accession: A37073  
 A;Molecule type: mRNA  
 A;Residues: 1-467 <HAS>  
 A;Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAAB8021.1; PID:G180618  
 R;Devraj, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.  
 Blood 77, 2731-2738, 1991  
 A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.  
 A;Reference number: A61175; MUID:91255696; PMID:1646048  
 A;Accession: A61175  
 A;Status: not compared with conceptual translation  
 A;Molecule type: protein  
 A;Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>  
 A;Accession: B61175  
 A;Molecule type: protein  
 A;Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>  
 R;Maliya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V  
 Biochemistry 29, 10628-10634, 1990  
 A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with  
 A;Reference number: A36230; MUID:91104978; PMID:2178876  
 A;Accession: A36230  
 A;Molecule type: protein  
 A;Residues: 'X', 86-87, 'X', 89-90, 'X', 92-97, 'X', 99-111, 'X', 113-120 <MAL>  
 R;Knauper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
 Eur. J. Biochem. 189, 295-300, 1990  
 A;Title: Characterization and activation of procollagenase from human polymorphonuclear  
 A;Reference number: S03680; MUID:90249372; PMID:2159879  
 A;Accession: S03680  
 A;Molecule type: protein  
 A;Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-1  
 A;Note: 67-Lys was also found  
 R;Knauper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
 Biol. Chem. Hoppe-Seyler 371, 733, 1990  
 A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.  
 A;Reference number: S11026; MUID:91000455; PMID:2169786  
 A;Note: original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990  
 A;Accession: S11026  
 A;Molecule type: protein  
 A;Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140; 183-203, 'X', 205-209; 248-261  
 A;Note: 87-Glu was also found  
 R;Blaeser, J.; Knauper, V.; Osthus, A.; Reinke, H.; Tschesche, H.  
 Eur. J. Biochem. 202, 1223-1230, 1991  
 A;Title: Mercurial activation of human polymorphonuclear leukocyte procollagenase.  
 A;Reference number: S19576; MUID:92111500; PMID:1662606  
 A;Accession: S19576  
 A;Molecule type: protein  
 A;Residues: 69-103 <BL2>  
 R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.  
 FEBS Lett. 313, 59-61, 1992  
 A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procoll  
 A;Reference number: S27225; MUID:93050220; PMID:1330697  
 A;Accession: S27225  
 A;Molecule type: protein  
 A;Residues: 68-103 <BLA>  
 R;Knauper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Tschesche, H.  
 Biochem. J. 291, 847-854, 1993  
 A;Title: Fragmentation of human polymorphonuclear-leukocyte collagenase.  
 A;Reference number: S32527; MUID:93256897; PMID:8489511  
 A;Accession: S32527  
 A;Molecule type: protein  
 A;Residues: 100-112; 263-276 <KN3>  
 R;Knauper, V.; Murphy, G.; Tschesche, H.  
 Eur. J. Biochem. 235, 187-193, 1996  
 A;Title: Activation of human neutrophil procollagenase by stromelysin 2.  
 A;Reference number: S62608; MUID:96202934; PMID:8631328  
 A;Accession: S62608  
 A;Molecule type: protein  
 A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>  
 R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.  
 submitted to the Brookhaven Protein Data Bank, January 1994  
 A;Reference number: A67078; FDB:IMNC  
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 'I'

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, Nat. Struct. Biol. 1, 119-123, 1994  
 A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.  
 A;Reference number: A58274; MUID:95384762; PMID:7656015  
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 'I'  
 C;Comment: This protein is more highly glycosylated than interstitial collagenase and is  
 C;Genetics:  
 A;Gene: GDB:MMP8; CLG1  
 A;Cross-references: GDB:128173; OMIM:120355  
 A;Map position: 11q22.2-11q22.3  
 C;Function:  
 A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous  
 A;Note: Cleaves type I collagen most rapidly  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein  
 C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-467/Product: procollagenase #status predicted <PRO>  
 F;21-100/Domain: activation peptide #status experimental <ACT>  
 F;59-262/Domain: matrix metalloproteinase homology <MMP>  
 F;89-96/Region: autoinhibitory  
 F;101-467/Product: neutrophil collagenase #status predicted <MAT>  
 F;123-464/Domain: hemopexin repeat homology <PXN>  
 F;54,73,112,119,204,246/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;73-74/Cleavage site: Asn-Val (autolytic) #status experimental  
 F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental  
 F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
 F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental  
 F;167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime  
 F;174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e  
 F;217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental  
 F;218/Active site: Glu #status predicted  
 F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental  
 F;279-464/Disulfide bonds: #status predicted  
 Query Match 73.3%; Score 214; DB 1; Length 467;  
 Best Local Similarity 70.4%; Pred. No. 1,2e-18;  
 Matches 38; Conservativity 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MQEFGKVTGKDPDABTLKMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 66 MQEFGKVTGKDPDABTLKMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 119  
 RESULT 7  
 KCHUS2  
 stromelysin 2 (EC 3.4.24.22) precursor [validated] - human  
 N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: A28816; A47496  
 R;Mueller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988  
 A;Title: The collagenase gene family in humans consists of at least four members.  
 A;Reference number: A90339; MUID:88339885; PMID:2844164  
 A;Accession: A28816  
 A;Molecule type: mRNA  
 A;Residues: 1-476 <MUL>  
 A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:936628; PIDN:CAA30679.1; PID:G36629  
 A;Note: mRNA for this protein was detected in several human tumors  
 R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal- J. Biol. Chem. 268, 17341-17347, 1993  
 A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gen  
 A;Reference number: A47496; MUID:93352520; PMID:8349617  
 A;Accession: A47496  
 A;Molecule type: protein  
 A;Residues: 17-33 <WIN>  
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
 C;Genetics:  
 A;Gene: GDB:MMP10; STMY2  
 A;Cross-references: GDB:120392; OMIM:185260  
 A;Map position: 11q22.3-11q23  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein  
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

Biochemistry 37, 4699-4702, 1998

A>Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1  
A:Reference number: A58912; MUID:9548733; PMID:9548733  
A:Contents: annotation  
R:Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, February 1997

A:Reference number: A68466; PDB:1KFS  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160  
R:Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.  
Protein Sci. 4, 1966-1976, 1995

A>Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain  
A:Reference number: A58914; MUID:96117647; PMID:8535233  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms  
R:Marcy, A.I.; Elberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.; Eschbach, S.P.; Salowe, G.C.; Cucu, A.I.; Gagliardi, C.A.; Johnson, B.A.; Marcy, A.I.  
Biochemistry 32, 13098-14008, 1993

A>Title: Secondary structure and zinc ligation of human recombinant short-form stromelysin  
A:Contents: annotation; conformation by (1)H-NMR, residues 100-272  
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation site  
C:Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of which are active  
C:Genetics:  
A:Gene: GDB:MMP3; STWY; STMV1  
A:Cross-references: GDB:120727; OMIM:185250  
A:Map position: 1lq23-1lq23  
C:Function:

A>Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side  
A>Note: degrades various extracellular matrix proteins, including fibronectin, plasminogen, plasminogen to yield a fragment with angiotensin activity  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallic  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-477/Product: prostromelysin 1 #status experimental <PRO>  
F:18-99/Domain: activation peptide #status experimental <ACT>  
F:60-264/Domain: matrix metalloproteinase homology <MMP>  
F:100-477/Product: stromelysin 1 #status experimental <MAT>  
F:284-477/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His)  
F:210/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
F:219/Active site: Glu #status predicted  
F:290-477/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 477;  
Best Local Similarity 63.0%; Pred. No. 1.6e-15;  
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MQEFGGLVKVTGPKDAETLKNMKRCQGVDPVAQFVLTEGNPRWEQTHLYRIEN 54  
Db 67 MQEFLGLEVTGKLSDTLEVMRKPCQGVDPVGHFRTFPGIKWRKTHLYRIVN 120

RESULT 9  
XCRBS1  
N:Alcarnate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3);  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A37366; A29157  
R:Finli, M.E.; Karmaliowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckhoff,  
Arthritis Rheum. 30, 1254-1264, 1987









GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 49.8462 Seconds  
(without alignments)  
623.323 Million cell updates/sec

Title: US-10-032-376A-9  
Perfect score: 292  
Sequence: 1 MQEFFGLKVTGKPAETLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1606865

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:\*

1: uniprot\_prot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	469	1 MM01 HUMAN	P03956 homo sapien
2	292	100.0	469	2 AAP3520	Aap3520 homo sapi
3	283	96.9	468	1 MM01 RABIT	P13943 oryctolagus
4	279	95.5	469	1 MM01 HORSE	Q9X825 equus caball
5	270	92.5	469	1 MM01 PIG	P21692 sus scrofa
6	234	80.1	469	1 MM01 BOVIN	P28053 bos taurus
7	231.5	79.3	384	1 MM01 RANCA	Q11133 rana catesb
8	214	73.3	467	1 MM08 HUMAN	P22894 homo sapien
9	204	69.9	205	2 Q810Z2	Q810Z2 mus musculu
10	204	69.9	463	2 Q9EPL6	Q9EPL6 mus musculu
11	204	69.9	464	2 Q9EPL5	Q9EPL5 mus musculu
12	196	67.1	466	1 MM08 RAT	O88766 rattus norv
13	189	64.7	476	1 MM10 HUMAN	P09238 homo sapien
14	189	64.7	476	2 AAP36110	Aap36110 homo sapi
15	189	64.7	477	1 MM03 HUMAN	P08254 homo sapien
16	189	64.7	477	2 AAH65676	Aah65676 homo sapi
17	189	64.7	477	2 AAH69716	Aah69716 homo sapi
18	189	64.7	478	2 Q6Y4Q5	Q6Y4Q5 canis faml
19	189	64.7	478	2 AAOC3580	Aaoc3580 canis fam
20	186	63.7	145	2 Q9N283	Q9N283 bos taurus
21	186	63.7	393	2 Q8MI18	Q8MI18 felis silve
22	186	63.7	478	1 MM03 RABIT	P28863 oryctolagus
23	184	63.0	252	2 Q6PWQ3	Q6PWQ3 xenopus lae
24	184	63.0	252	2 AAT00547	Aat00547 xenopus l
25	184	63.0	259	2 Q7ZTI9	Q7ZTI9 xenopus lae
26	183	62.7	472	2 Q93342	Q93342 gallus gall
27	183	62.7	477	1 MM03 HORSE	Q28397 equus caball
28	181	62.0	466	2 Q7SYX1	Q7SYX1 xenopus lae
29	180	61.6	259	2 Q7SXT5	Q7SXT5 xenopus lae
30	179	61.3	458	2 Q6DCN8	Q6DCN8 xenopus lae
31	178	61.0	258	2 Q7S2S8	Q7S2S8 xenopus lae

RESULT 1	MM01_HUMAN	STANDARD;	PRT;	469 AA.
ID	MM01_HUMAN			
AC	P03956; P08156;			
DT	23-OCT-1986 (Rel. 02, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix			
DE	metalloproteinase-1) (MMP-1) (Fibroblast collagenase).			
GN	Name=MMPI; Synonyms=CLG;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=90352587; PubMed=2167156;			
RA	Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,			
RA	Stetler-Stevenson W.G.;			
RT	"Cloning and characterization of human tumor cell interstitial			
RT	collagenase.";			
RL	Cancer Res. 50:5431-5437(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=87156645; PubMed=3030290;			
RA	Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,			
RA	Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;			
RT	"Comparison of human stromelysin and collagenase by cloning and			
RT	sequence analysis.";			
RL	Biochem. J. 240:913-916(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=86196089; PubMed=3009463;			
RA	Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,			
RA	Eisen A.Z.;			
RT	"Human fibroblast collagenase. Complete primary structure and homology			
RT	to an oncogene transformation-induced rat protein.";			
RL	J. Biol. Chem. 261:6600-6605(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,			
RA	Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,			
RA	Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,			
RA	Heller R., Davis R.W.;			
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Ovary;			
RC	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

Q6df35 xenopus tro  
O18767 bos taurus  
Q8c209 mus musculu  
Q8c230 mus musculu  
Aah42742 mus muscu  
Bac40805 mus muscu  
O62806 oryctolagus  
Q7zwd0 brachydanic  
P57748 mus musculu  
O55123 mus musculu  
P28862 mus musculu  
Q922w6 mus musculu  
P03957 rattus norv  
O60882 homo sapien

## ALIGNMENTS

RA Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP SEQUENCE OF 1-35 FROM N.A.  
RX MEDLINE=87257941; PubMed=3037355;  
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,  
RA Herrlich P.,  
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human  
RT collagenase gene is mediated by an inducible enhancer element located  
RT in the 5'-flanking region.";  
RL Mol. Cell. Biol. 7:2256-2266(1987).  
RN [7]  
RP SEQUENCE OF 1-70 FROM N.A.  
RC TISSUE-Synovial cell;  
RX MEDLINE=87109799; PubMed=3027129;  
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;  
RT "Molecular cloning of human synovial cell collagenase and selection of  
RT a single gene from genomic DNA.";  
RL J. Clin. Invest. 79:542-546(1987).  
RN [8]  
RP SEQUENCE OF 100-112 AND 270-287.  
RC TISSUE=Fibroblast;  
RX MEDLINE=90104231; PubMed=2557822;  
RA Clark I.M., Cawston T.E.;  
RT "Fragments of human fibroblast collagenase. Purification and  
RT characterization.";  
RL Biochem. J. 263:201-206(1989).  
RN [9]  
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.  
RX MEDLINE=87194799; PubMed=3032950;  
RA McKerrow J.H.;  
RT "Human fibroblast collagenase contains an amino acid sequence  
RT homologous to the zinc-binding site of Serratia protease.";  
RL J. Biol. Chem. 262:5943-5943(1987).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.  
RX MEDLINE=95384760; PubMed=7656013;  
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,  
RA Brown P.A., Johnson W.H., Murray E.J.;  
RT "Structure of the catalytic domain of human fibroblast collagenase  
RT complexed with an inhibitor.";  
RL Nat. Struct. Biol. 1:106-110(1994).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.  
RX MEDLINE=94304829; PubMed=8031754;  
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;  
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase  
RT complexed to itself.";  
RL Biochemistry 33:8207-8217(1994).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.  
RX MEDLINE=94105765; PubMed=8278810;  
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,  
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,  
RA Jordan S.R.;  
RT "Structure of the catalytic domain of fibroblast collagenase complexed  
RT with an inhibitor.";  
RL Science 263:375-377(1994).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.

RX MEDLINE=94377426; PubMed=8090713;  
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,  
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;  
RT "1.56-A structure of mature truncated human fibroblast collagenase.";  
RL Proteins 19:98-109(1994).  
RN [14]  
RP STRUCTURE BY NMR OF 101-269.  
RX MEDLINE=98145213; PubMed=9484219;  
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,  
RA Powers R.;  
RT "High-resolution solution structure of the inhibitor-free catalytic  
RT fragment of human fibroblast collagenase determined by  
RL Biochemistry 37:1495-1504(1998).  
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
CC the helical domain. Also cleaves collagens of types VII and X.  
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
CC collagen. Cleavage of the triple helix of collagen at about three-  
CC quarters of the length of the molecule from the N-terminus, at  
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
CC substrates and alpha-macroglobulins at bonds where P1' is a  
CC hydrophobic residue.  
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -!- ENZYME REGULATION: Can be activated without removal of the  
CC activation peptide.  
CC -!- DOMAIN: There are two distinct domains in this protein; the  
CC catalytic N-terminal, and the C-terminal which is involved in  
CC substrate specificity and in binding TIMP (tissue inhibitor of  
CC metalloproteinases).  
CC -!- PMW: Undergoes autocatalytic cleavage to two major forms (22 kDa and  
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22  
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form  
CC can act as activator for collagenase.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
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CC -----  
EMBL; X05231; CAA28858.1; -  
DR EMBL; M13509; AAA35699.1; -  
DR EMBL; M16567; AAA32033.1; -  
DR EMBL; U78045; AAB36941.1; -  
DR EMBL; BC013875; AAH13875.1; -  
DR EMBL; M15996; AAA35700.1; -  
DR EMBL; X54925; CAA38691.1; -  
DR PIR; A37308; KCHUI  
DR PDB; 1AYK; NMR; @=101-269.  
DR PDB; 1CGE; X-ray; @=102-269.  
DR PDB; 1CGF; X-ray; A/B=102-263.  
DR PDB; 1HFC; X-ray; A/B=101-269.  
DR PDB; 2AYK; NMR; @=101-269.  
DR PDB; 2TCL; X-ray; @=101-269.  
DR PDB; 3AYK; NMR; A=101-269.  
DR PDB; 4AYK; NMR; A=101-269.  
DR MEROPS; M10.001; -  
DR GlycoSuiteDB; P03956; -  
DR Genew; HGNC:7155; MMP1.  
DR MTM; 120353; -  
DR GO; GO:0008133; F:collagenase activity; TAS.  
DR GO; GO:0008270; F:zinc ion binding; TAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR001818; Pept M10A M12B.  
DR InterPro; IPR006025; Pept M Zn\_BS.  
DR InterPro; IPR009070; PGSD\_Like.

DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.

Query Match 100.0%; Score 292; DB 1; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-29;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 DB 67 MQEFGGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 2  
 ID AAF35520 PRELIMINARY; PRT; 469 AA.  
 AC AAF35520;  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Matrix metalloproteinase 1 (interstitial collagenase).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Carnivora; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
 RA Phelan M., Farmer A.;  
 RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
 vector."  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT006874; AAF35520.1; -;  
 KW Collagen.  
 SQ SEQUENCE 469 AA; 54007 MW; 4B1361DCF4C54B20 CRC64;

Query Match 100.0%; Score 292; DB 2; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-29;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 DB 67 MQEFGGLKVTGKPDAAETLKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 3  
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 AC P13943;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
 metalloproteinase-1) (MMP-1).  
 GN Name=MMP1;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Synovial cell;  
 RA MEDLINE=88077876; PubMed=2825772;  
 RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;  
 RT "A gene for rabbit synovial cell collagenase; member of a family of  
 metalloproteinases that degrade the connective tissue matrix."  
 RL Biochemistry 26:6156-6165 (1987).  
 RN [2]  
 RP SEQUENCE OF 449-468 FROM N.A.  
 RA STRAIN=New Zealand white;  
 RA MEDLINE=87029174; PubMed=3021384;  
 RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,  
 RA Brinckerhoff C.E.;

"Homology between exon-containing portions of rabbit genomic clones  
 for synovial cell collagenase and human foreskin and synovial cell  
 mRNAs.";  
 Coll. Relat. Res. 6:239-248 (1986).  
 CC FUNCTION: Cleaves collagens of types I, II, and III at one site in  
 the helical domain. Also cleaves collagens of types VII and X.  
 CC CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 collagen. Cleavage of the triple helix of collagen at about three-  
 quarters of the length of the molecule from the N-terminus, at  
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 substrates and alpha-macroglobulins at bonds where Pl' is a  
 hydrophobic residue.  
 CC COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By  
 similarity).  
 CC ENZYME REGULATION: Can be activated without removal of the  
 activation peptide.  
 CC SIMILARITY: Belongs to peptidase family M10A.  
 CC SIMILARITY: Contains 1 hemopexin-like domain.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 EMBL; M17823; AAB88016.1; -;  
 EMBL; M17820; AAB88016.1; JOINED.  
 EMBL; M17821; AAB88016.1; JOINED.  
 EMBL; M17822; AAB88016.1; JOINED.  
 EMBL; M19240; AAB88016.1; JOINED.  
 EMBL; M25663; AAB31203.1; -;  
 PIR; A27500; KCRBI.  
 DR HSSP; P03956; ICGL.  
 DR MEROPS; M10.001; -;  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGSD\_like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZmC; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Calcium-binding; Collagen degradation; Extracellular matrix;  
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
 Zymogen.  
 FT SIGNAL 1 18  
 FT PROPEP 19 98  
 FT CHAIN 99 468  
 FT DOMAIN 274 468  
 FT SITE 91 91  
 FT METAL 123 123  
 FT METAL 157 157  
 FT METAL 167 167  
 FT METAL 169 169  
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 FT METAL 177 177  
 FT METAL 179 179  
 FT METAL 182 182  
 FT METAL 189 189  
 FT METAL 191 191

Activation peptide.  
 Interstitial collagenase.  
 Hemopexin-like.  
 Cysteine switch (Potential).  
 Calcium 1 (By similarity).  
 Calcium 2 (By similarity).  
 Zinc 1 (By similarity).  
 Zinc 1 (By similarity).  
 Calcium 3 (By similarity).  
 Calcium 3 (via carbonyl oxygen) (By  
 similarity).  
 Calcium 3 (via carbonyl oxygen) (By  
 similarity).  
 Calcium 3 (via carbonyl oxygen) (By  
 similarity).  
 Zinc 1 (By similarity).  
 Calcium 2 (via carbonyl oxygen) (By  
 similarity).  
 Calcium 2 (via carbonyl oxygen) (By  
 similarity).

```

FT METAL 193 193 similarity).
FT METAL 195 195 Calcium 2 (By similarity).
FT METAL 197 197 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 200 200 Calcium 3 (By similarity).
FT METAL 217 217 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 218 218 By similarity.
FT METAL 221 221 Zinc 2 (catalytic) (By similarity).
FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
FT METAL 284 284 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 328 328 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 377 377 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 426 426 Calcium 4 (via carbonyl oxygen) (By similarity).
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Probable).
FT DISULFID 277 465 By similarity.
SQ SEQUENCE 468 AA; 53739 MW; DA905389195288C CRC64;

Query Match 96.9%; Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 1.2e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDAAETLKVMKQPRCGVDPVAFVLTGPNRWEQTHLYRIEN 54
Db 66 MQBFFGLKVTGKPDAAETLKVMKQPRCGVDPVAFVLTGPNRWEQTHLYRIEN 119

RESULT 4
MM01 HORSE
ID MM01 HORSE STANDARD; PRT; 469 AA.
AC QXASZ5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT Cloning and expression of equine matrix metalloproteinase 1 (interstitial collagenase).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the activation peptide.
CC -1- SIMILARITY: Belongs to peptidase family M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC EMBL; AF148882; AAD38030.1; -.
DR HSSP; P03956; 1AYK.
DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 99 Activation peptide.
FT CHAIN 100 469 Interstitial collagenase.
FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 92 Cysteine switch (potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 199 199 Calcium 1 (By similarity).
FT METAL 201 201 Calcium 3 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).
FT DISULFID 278 466 By similarity.
SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;

Query Match 95.5%; Score 279; DB 1; Length 469;
Best Local Similarity 94.4%; Pred. No. 3.9e-27;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MQBFFGLKVTGKPDAAETLKVMKQPRCGVDPVAFVLTGPNRWEQTHLYRIEN 54
Db 67 MQBFFGLKVTGKPDAAETLKVMKQPRCGVDPVAFVLTGPNRWEQTHLYRIEN 120

RESULT 5
MM01_PIG

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ID MM01\_PIG STANDARD; PRT; 469 AA.  
AC P21692;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
DE metalloproteinase-1) (MMP-1).  
GN Name:MMP1;  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
[1]  
RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RX MEDLINE=91333421; PubMed=1651440;  
RA Richards C.B., Rafferty J.A., Reynolds J.J., Saklatvala J.;  
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and  
RT modulation of expression of RNA in vitro by various cytokines.";  
RL Matrix 11:161-167(1991).  
[2]  
RN SEQUENCE OF '25-469 FROM N.A.  
RC TISSUE=Synovial cell;  
RX MEDLINE=91067477; PubMed=2174547;  
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;  
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,  
RT obtained by PCR.";  
RL Nucleic Acids Res. 18:6703-6703(1990).  
[3]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.  
RX MEDLINE=96173003; PubMed=8590015;  
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,  
RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;  
RT "Structure of full-length porcine synovial collagenase reveals a C-  
RT terminal domain containing a calcium-linked, four-bladed beta-  
RT propeller.";  
RL Structure 3:541-549(1995).  
[4]  
RN SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.  
RX MEDLINE=95142615; PubMed=7840605;  
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,  
RA O'Hare M.C.;  
RT "Recombinant porcine collagenase: purification and autolysis.";  
RL Arch. Biochem. Biophys. 316:123-127(1995).  
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
CC the helical domain. Also cleaves collagens of types VII and X.  
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
CC collagen. Cleavage of the triple helix of collagen at about three-  
CC quarters of the length of the molecule from the N-terminus, at  
CC 775-Gly-118-776 in the alpha-1(I) chain. Cleaves synthetic  
CC substrates and alpha-macroglobulins at bonds where P1' is a  
CC hydrophobic residue.  
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -1- ENZYME REGULATION: Can be activated without removal of the  
CC activation peptide.  
CC -1- PTM: Undergoes autocatalytic cleavage to produce a N-terminal fragment  
CC having reduced collagenolytic activity.  
CC -1- SIMILARITY: Belongs to peptidase family M10A.  
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC -----  
DR EMBL; X54724; CAA38526.1; -  
DR PDB; 1S1986; KCPGI.  
DR PDB; 1FBL; X-ray; @=100-469.  
DR MEROPS; M10.001; -  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase\_M.

DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR009070; PGSD\_Like.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PRC0138; MATRININ.  
DR SMART; SMO0130; HX; 4.  
DR SMART; SMO0235; ZMNC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR 3D-structure; Autocatalytic cleavage; Calcium-binding;  
KW Collagen degradation; Direct protein sequencing; Extracellular matrix;  
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
KW Zymogen.  
FT SIGNAL 1 19  
FT PROPEP 20 99 Activation peptide.  
FT CHAIN 100 469 Interstitial collagenase.  
FT CHAIN 100 258 18 kDa interstitial collagenase.  
FT DOMAIN 275 469 Hemopexin-like.  
FT SITE 92 Cysteine switch (Potential).  
FT SITE 258 259 Cleavage (autolytic).  
FT METAL 124 124 Calcium 1.  
FT METAL 158 158 Calcium 2.  
FT METAL 168 168 Zinc 1.  
FT METAL 170 170 Zinc 1.  
FT METAL 175 175 Calcium 3.  
FT METAL 176 176 Calcium 3 (via carbonyl oxygen).  
FT METAL 178 178 Calcium 3 (via carbonyl oxygen).  
FT METAL 180 180 Calcium 3 (via carbonyl oxygen).  
FT METAL 183 183 Zinc 1.  
FT METAL 190 190 Calcium 2 (via carbonyl oxygen).  
FT METAL 192 192 Calcium 2 (via carbonyl oxygen).  
FT METAL 194 194 Calcium 2.  
FT METAL 196 196 Zinc 1.  
FT METAL 198 198 Calcium 3.  
FT METAL 199 199 Calcium 1.  
FT METAL 201 201 Calcium 3.  
FT METAL 218 218 Zinc 2 (catalytic).  
FT ACT\_SITE 219 219  
FT METAL 222 222 Zinc 2 (catalytic).  
FT METAL 228 228 Zinc 2 (catalytic).  
FT METAL 285 285 Calcium 4 (via carbonyl oxygen).  
FT METAL 329 329 Calcium 4 (via carbonyl oxygen).  
FT METAL 378 378 Calcium 4 (via carbonyl oxygen).  
FT METAL 427 427 Calcium 4 (via carbonyl oxygen).  
FT METAL 466 466  
FT DISULFID 278 466  
FT CARBOHYD 120 120 N-linked (GlcNAc... ) (Potential).  
FT STRAND 101 102  
FT TURN 104 105  
FT STRAND 113 118  
FT TURN 123 124  
FT TURN 127 142  
FT HELIX 143 144  
FT TURN 148 152  
FT STRAND 159 164  
FT STRAND 182 184  
FT TURN 190 193  
FT STRAND 195 198  
FT TURN 199 200  
FT STRAND 204 204  
FT STRAND 211 211  
FT STRAND 212 223  
FT TURN 224 225  
FT STRAND 226 227  
FT TURN 232 233  
FT TURN 235 236  
FT HELIX 250 260  
FT TURN 277 278  
FT TURN 280 281  
FT STRAND 286 290  
FT TURN 291 292

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FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT STRAND 335 338
FT TURN 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT STRAND 364 368
FT HELIX 372 373
FT STRAND 379 383
FT TURN 384 387
FT STRAND 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D2B2753F682 CRC64;

Query Match 92.5%; Score 270; DB 1; Length 469;
Best Local Similarity 90.7%; Pred. No. 5.5e-26;
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKDAETLKVMKQPCGVDPAQFVLTEGNPRWEQHLTYRIEN 54
Db 67 MQOFFGLKVTGKDAETLNVMKQPCGVDPAEAFVLTGPNRWENTHLTYRIEN 120

RESULT 6
MM01_BOVIN STANDARD; PRT; 469 AA.
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periodontium fibroblast;
RX MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence.";
RL DNA Seq. 5:63-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=1311165;

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RA Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D., Parks W.C.;  
 RA "Purification and characterization of bovine interstitial collagenase and tissue inhibitor of metalloproteinases."; Arch. Biochem. Biophys. 293:370-376(1992).  
 RL Arch. Biochem. Biophys. 293:370-376(1992).  
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).  
 CC -!- ENZYME REGULATION: Can be activated without removal of the activation peptide.  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
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 CC -----  
 DR EMBL; X58256; CAA41210.1; --  
 DR PIR; S14654; KCBOL.  
 DR HSSP; P03956; IHFC.  
 DR MEROPS; M10.001; --  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR01818; Pept\_M10A\_M12B.  
 DR InterPro; IPR004025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PQBD\_like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SMC0235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR Calcium-binding; Collagen degradation; Direct protein sequencing;  
 KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;  
 KW Metalloprotease; Signal; Zinc; zymogen.  
 FT SIGNAL 1 18  
 FT PROPEP 19 99 Activation peptide.  
 FT CHAIN 100 469 Interstitial collagenase.  
 FT DOMAIN 275 469 Hemopexin-like.  
 FT SITE 92 92 Cysteine switch (Potential).  
 FT METAL 124 124 Calcium 1 (By similarity).  
 FT METAL 158 158 Calcium 2 (By similarity).  
 FT METAL 168 168 Zinc 1 (By similarity).  
 FT METAL 170 170 Zinc 1 (By similarity).  
 FT METAL 175 175 Calcium 3 (By similarity).  
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 183 183 Zinc 1 (By similarity).  
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 194 194 Calcium 2 (By similarity).  
 FT METAL 196 196 Zinc 1 (By similarity).  
 FT METAL 198 198 Calcium 3 (By similarity).



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FT METAL 199 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 201 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 218 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT ACT SITE 219 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 222 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 228 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 285 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 329 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 378 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT METAL 427 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT DISULFID 278 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CARBOHYD 120 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 22 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 30 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 35 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 85 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 106 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
FT CONFLICT 113 329 427 466 278 120 120 23 30 36 85 108 113 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;
SQ SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;

Query Match 80.1%; Score 234; DB 1; Length 469;
Best Local Similarity 81.5%; Pred. No. 2.4e-21;
Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 67 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120

RESULT 7
MM01_RANCA STANDARD; PRT; 384 AA.
ID MM01_RANCA STANDARD; PRT; 384 AA.
AC Q11133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (TIMP-1) (TCL).
OS Rana catesbeiana (Bull frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Anura; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=95071832; Pubmed=7981043;
RA Oofusa K., Yomori S., Yoshizato K.;
RT "Regionally and hormonally regulated expression of genes of collagen and collagenase in the anuran larval skin.";
RL Int. J. Dev. Biol. 38:345-350(1994).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the activation peptide (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
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CC -----
CC EMBL; S75623; AAB32661.1; -.
CC PIR; I51267; I51267.
CC HSSP; P21692; 1FEL.
CC MEROPS; M10.001; -.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR001818; Pept M10.M12B.
CC InterPro; IPR006025; Pept M Zn BS.
CC InterPro; IPR009070; PGD-like.
CC Pfam; PF00045; Hemopexin; 2.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00138; MATRILIN.
CC SMART; SM00120; HX; 2.
CC SMART; SM00235; ZmG; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
CC PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Extracellular matrix;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 25 Potential.
FT PROPEP 26 88 Activation peptide (Potential).
FT CHAIN 89 384 Interstitial collagenase.
FT DOMAIN 239 384 Hemopexin-like.
FT SITE 81 81 Cysteine switch (Potential).
FT METAL 113 113 Calcium 1 (By similarity).
FT METAL 129 129 Calcium 2 (By similarity).
FT METAL 139 139 Zinc 1 (By similarity).
FT METAL 141 141 Zinc 1 (By similarity).
FT METAL 146 146 Calcium 3 (By similarity).
FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Calcium 3 (By similarity).
FT METAL 170 170 Calcium 1 (By similarity).
FT METAL 172 172 Calcium 3 (By similarity).
FT METAL 189 189 Zinc 2 (catalytic) (By similarity).
FT ACT SITE 190 190 By similarity.
FT METAL 193 193 Zinc 2 (catalytic) (By similarity).
FT METAL 199 199 Zinc 2 (catalytic) (By similarity).
FT METAL 249 249 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 277 277 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 347 347 Calcium 4 (via carbonyl oxygen) (By similarity).
FT DISULFID 242 381 By similarity.
SQ SEQUENCE 384 AA; 43582 MW; A5B5E3FB33239DF CRC64;

Query Match 79.3%; Score 231.5; DB 1; Length 384;
Best Local Similarity 79.6%; Pred. No. 4e-21;
Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 MQEFTGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 57 LKQFFGLKVTGKPDATLTKVMPKPCGVPDVAQFVLTGPNRWEQTHLYRIEN 109

RESULT 8

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MM08 HUMAN  
ID \_MM08 HUMAN STANDARD; PRT; 467 AA.  
AC P22854;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix  
DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).  
GN Name=MMP8; Synonyms=CLG1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1] \_SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.  
RN RP TISSUE=Neutrophils;  
RC MEDLINE=90307647; PubMed=2164002;  
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,  
RA Spinella D.G., Stevens R.M., Mainardi C.L.;  
RT "Human neutrophil collagenase. A distinct gene product with homology  
RT to matrix metalloproteinases.";  
RL J. Biol. Chem. 265:11421-11424(1990).  
[2]  
RN RP SEQUENCE OF 21-140.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90249372; PubMed=2159879;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RT "Characterization and activation of procollagenase from human  
RT polymorphonuclear leukocytes. N-terminal sequence determination of the  
RT proenzyme and various proteolytically activated forms.";  
RL Eur. J. Biochem. 189:295-300(1990).  
[3]  
RN RP SEQUENCE OF 21-103.  
RC TISSUE=Neutrophils;  
RX MEDLINE=92111500; PubMed=1662606;  
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;  
RT "Mercurial activation of human polymorphonuclear leukocyte  
RT procollagenase.";  
RL Eur. J. Biochem. 202:1223-1230(1991).  
[4]  
RN RP SEQUENCE OF 85-120, AND CHARACTERIZATION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91104978; PubMed=2176876;  
RA Mallva S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,  
RA Birkedal-Hansen H., van Wart H.B.;  
RT "Characterization of 58-kilodalton human neutrophil collagenase:  
RT comparison with human fibroblast collagenase.";  
RL Biochemistry 29:10628-10634(1990).  
[5]  
RN RP PARTIAL SEQUENCE.  
RX MEDLINE=90380298; PubMed=2169256;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";  
RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).  
[6]  
RN RP ERRATUM.  
RX MEDLINE=91000455; PubMed=2169766;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).  
[7]  
RN RP CYSTEINE-SWITCH MECHANISM.  
RC TISSUE=Neutrophils;  
RX MEDLINE=93050220; PubMed=1330697;  
RA Blaesser J., Triebel S., Reinke H., Tschesche H.;  
RT "Formation of a covalent Hg-Cys-bond during mercurial activation of  
RT PMNL procollagenase gives evidence of a cysteine-switch mechanism.";  
RL FEBS Lett. 313:59-61(1992).  
[8]  
RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.  
RX MEDLINE=94185631; PubMed=8137810;  
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;  
RT "The X-ray crystal structure of the catalytic domain of human  
RT neutrophil collagenase inhibited by a substrate analogue reveals the

essentials for catalysis and specificity.";  
RL EMBO J. 13:1263-1269(1994).  
[9]  
RN RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.  
RX MEDLINE=94139930; PubMed=8307185;  
RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,  
RA Tschesche H., Bode W.;  
RT "Structural implications for the role of the N terminus in the  
RT 'superactivation' of collagenases. A crystallographic study.";  
RL FEBS Lett. 338:227-233(1994).  
[10]  
RN RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.  
RX MEDLINE=95384762; PubMed=7656015;  
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,  
RA Oronfleh M.W., Banks T.M., Rubin B.;  
RT "Structure of human neutrophil collagenase reveals large S1'  
RT specificity pocket.";  
RL Nat. Struct. Biol. 1:119-123(1994).  
[11]  
RN RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.  
RX MEDLINE=97390108; PubMed=9249047;  
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,  
RA Bode W., Gomis-Ruth F.-X.;  
RT "1.8-A crystal structure of the catalytic domain of human neutrophil  
RT collagenase (matrix metalloproteinase-8) complexed with a  
RT peptidomimetic hydroxamate primed-side inhibitor with a distinct  
RT selectivity profile.";  
RL Eur. J. Biochem. 247:356-363(1997).  
[12]  
RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.  
RX MEDLINE=98318039; PubMed=9655333;  
RA Brandstetter H., Ergh R.A., von Roeder E.G., Moroder L., Huber R.,  
RA Bode W., Grams F.;  
RT "Structure of malonic acid-based inhibitors bound to human neutrophil  
RT collagenase. A new binding mode explains apparently anomalous data.";  
RL Protein Sci. 7:1303-1309(1998).  
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.  
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the  
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves  
CC type III collagen more slowly than type I.  
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.  
CC -!- ENZYME REGULATION: Cannot be activated without removal of the  
CC activation peptide.  
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.  
CC -!- TISSUE SPECIFICITY: Neutrophils.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
-----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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CC EMBL; J05556; AAA88021.1; -  
CC PIR; A37073; KCHUN  
DR PDB; 1A85; X-ray; A=105-262.  
DR PDB; 1A86; X-ray; A=105-262.  
DR PDB; 1B25; X-ray; A=99-263.  
DR PDB; 1I73; X-ray; A=100-262.  
DR PDB; 1I76; X-ray; A=100-262.  
DR PDB; 1JAN; X-ray; A=99-262.  
DR PDB; 1JAO; X-ray; A=100-262.  
DR PDB; 1JAF; X-ray; A=100-262.  
DR PDB; 1JAJ; X-ray; A=100-262.  
DR PDB; 1JU9; X-ray; A=105-262.  
DR PDB; 1JUB; X-ray; A=100-262.  
DR PDB; 1KBC; X-ray; A/B=99-262.  
DR PDB; 1MBB; X-ray; A=100-262.  
DR PDB; 1MNC; X-ray; @=101-263.  
DR MEROPS; M10.002; -.

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DR Genew; HGNC:7175; MMP8.
DR MW; 120355; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008330; F:neutrophil collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00433; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium_binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydroxylase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
DR SIGNAL 1 20
DR PROPEP 21 100 Activation peptide.
DR CHAIN 101 467 Neutrophil collagenase.
DR DOMAIN 276 467 Hemopexin-like.
DR SITE 91 91 Cysteine switch.
DR METAL 157 157 Calcium 1.
DR METAL 167 167 Zinc 1.
DR METAL 169 169 Zinc 1.
DR METAL 174 174 Calcium 2.
DR METAL 175 175 Calcium 2 (via carbonyl oxygen).
DR METAL 177 177 Calcium 2 (via carbonyl oxygen).
DR METAL 179 179 Calcium 2 (via carbonyl oxygen).
DR METAL 182 182 Zinc 1.
DR METAL 189 189 Calcium 1 (via carbonyl oxygen).
DR METAL 191 191 Calcium 1 (via carbonyl oxygen).
DR METAL 193 193 Calcium 1.
DR METAL 195 195 Zinc 1.
DR METAL 197 197 Calcium 2.
DR METAL 200 200 Calcium 2.
DR METAL 217 217 Zinc 2 (catalytic).
DR METAL 218 218 Zinc 2 (catalytic).
DR ACT SITE 221 221 Zinc 2 (catalytic).
DR METAL 221 221 Zinc 2 (catalytic).
DR METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
DR METAL 286 286 similarity).
DR METAL 378 378 Calcium 3 (via carbonyl oxygen) (By
DR METAL 425 425 similarity).
DR METAL 425 425 Calcium 3 (via carbonyl oxygen) (By
DR METAL 54 54 N-linked (GlcNAc. .) (Probable).
DR CARBOHYD 73 73 N-linked (GlcNAc. .) (Probable).
DR CARBOHYD 112 112 N-linked (GlcNAc. .) (Probable).
DR CARBOHYD 204 204 N-linked (GlcNAc. .) (Potential).
DR CARBOHYD 246 246 N-linked (GlcNAc. .) (Potential).
DR DISULFID 279 464 Probable.

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 8.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
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66 MQRFEGLVNTPKNEETLDMMKPKRCGVPDGGFMTFGNPKWERTNLTLYRIEN 119

RESULT 9
Q81022 PRELIMINARY; PRT; 205 AA.
AC Q81022
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).
```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Brathwaite M., Waelitz P., Nagaraja R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY211543; AAC37584.1; -.
DR MEROPS; M10_034; -.
DR CO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00235; ZnMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR NON_TER 205 205
KW Collagen.
SQ SEQUENCE 205 AA; 23403 MW; DBD1E974E8769643 CRC64;

Query Match 69.9%; Score 204; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 7.2e-18;
Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGPDATLKVMPKRCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
||| ||||| :||| :||| :||| :||| :||| :||| :||| :|||
64 MQQLFGLKVTGNSDPETLRANKKRCGVPDVAFYATHTNPRWTKHTLYSILN 117

RESULT 10
Q9EPL6 PRELIMINARY; PRT; 463 AA.
AC Q9EPL6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative matrix metalloproteinase.
GN Name=Mmp1b; Synonyms=McolB;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21167837; PubMed=1113146;
RA Balbin M., Fuyo A., Knauper V., Lopez J.M., Alvarez J., Sanchez L.M.,
RA Quesada V., Bordallo J., Murphy G., Lopez-Otin C.;
RL Identification and enzymatic characterization of two diverging murine
RT counterparts of human interstitial collagenase (MMP-1) expressed at
RT sites of embryo implantation.;
RL J. Biol. Chem. 276:10253-10262(2001).
DR EMBL; AJ278461; CAC18879.1; -.
DR HSSP; P08254; 1HY7.
DR MEROPS; M10_034; -.
DR MGD; MGI:1933847; Mmp1b.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001843; Pept_M10A_M10C.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF02051; Fragilysin; 1.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
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DR SMART; SMO0120; HX; 4.  
 DR SMART; SMO0235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 463 AA; 53492 MW; 46013AB9D106C3F1 CRC64;  
 Query Match 69.9%; Score 204; DB 2; Length 463;  
 Best Local Similarity 66.7%; Pred. No. 1.7e-17;  
 Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
 Y 1 MQEFGGLKVTGKPDATLKVYKQPCGVPDVAQFVLTEGPNRWEQHLTVRIEN 54  
 D 64 MQQLFGLKVTGNSDPETLRANKKPCGVPDVAFYATHNNPRWTKTLTYSILN 117

RESULT 11  
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 ID Q9EPL5  
 AC Q9EPL5  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Putative matrix metalloproteinase (Mus musculus 7 days embryo whole  
 DE body cDNA, RIKEN full-length enriched library, clone:C430029P05  
 DE product:collagenase-like A, full insert sequence) (Collagenase-like  
 DE A).  
 GN Name=Mmp1a; Synonyms=McolA, collagenase-like A;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21167837; PubMed=11113146;  
 RA Balbin M., Fuyo A., Knapur V., Lopez J.M., Alvarez J., Sanchez L.M.,  
 RA Quesada V., Bordin J., Murphy G., Lopez-Otin C.;  
 RA "Identification and enzymatic characterization of two diverging murine  
 RA counterparts of human interstitial collagenase (MMP-1) expressed at  
 RA sites of embryo implantation.";  
 RL J. Biol. Chem. 276:10253-10262(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RA "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:585-590(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RA The FANTOM Consortium;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RA 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RA prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [6]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto H., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
 RA Yoneda Y., Ishikawa T., Okawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume M.,  
 RA Hayashida K., Hayatsu N., Hitamoto K., Hiraoka T., Kasukawa T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Sakazume N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ;  
 RC Brathwaite M., Waeltz P., Nagaraja R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ278462; CAC18880.1; -  
 DR EMBL; AK049552; BAC33807.1; -  
 DR EMBL; AY211543; AAO37582.1; -  
 DR HSP; P08254; 1HY7.  
 DR MEROPS; M10.033; -  
 DR MGD; MGI:1933846; Mmp1a.  
 DR GO; GO:0008133; F:collagenase activity; IDA.  
 DR InterPro; IPR000585; Hemoexin.  
 DR InterPro; IPR006026; Peptidase\_M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGSD\_like.  
 DR Pfam; PF00045; Hemoexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00138; MATRININ.  
 DR SMART; SMO0120; HX; 4.  
 DR SMART; SMO0235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 KW Collagen.  
 SQ SEQUENCE 464 AA; 53488 MW; 09FFC0470E5F9948 CRC64;  
 Query Match 69.9%; Score 204; DB 2; Length 464;  
 Best Local Similarity 66.7%; Pred. No. 1.7e-17;  
 Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
 Y 1 MQEFGGLKVTGKPDATLKVYKQPCGVPDVAQFVLTEGPNRWEQHLTVRIEN 54  
 D 64 MQQLFGLKVTGNSDPETLRANKKPCGVPDVAFYATHNNPRWTKTLTYSILN 117

RESULT 12

NM08\_RAT

ID NM08\_RAT

AC O88766;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix  
DE metalloproteinase-8) (MMP-8).  
GN Name=Mmp8;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RN SEQUENCE FROM N.A.  
RA STRAIN=Lewis;  
RA Overall C.M., Lowe D., Wells G., Clements J.M.;  
RT "cloning, expression, characterization and activation properties of  
RT rat neutrophil collagenase (MMP-8).";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: Can degrade fibrillar type I, II, and III collagens.  
CC -|- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the  
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves  
CC type III collagen more slowly than type I.  
CC -|- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By  
CC similarity).  
CC -|- ENZYME REGULATION: Cannot be activated without removal of the  
CC activation peptide (By similarity).  
CC -|- SUBCELLULAR LOCATION: Stored in intracellular granules.  
CC -|- SIMILARITY: Belongs to peptidase family M10A.  
CC -|- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AJ007288; CAA07432.1; -;  
CC HSP; P22894; 1B2S.  
DR MEROPS; M10.002; -;  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_Mzn\_BS.  
DR InterPro; IPR009070; PGSD-like.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00138; MATRIXIN.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
DR Calcium-binding; Collagen degradation; Extracellular matrix;  
DR Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
KW Zymogen.  
FT SIGNAL 1 20 By similarity.  
FT PROPEP 21 101 Activation peptide (By similarity).  
FT CHAIN 102 466 Neutrophil collagenase.  
FT DOMAIN 277 466 Hemopexin-like.  
FT SITE 92 92 Cysteine switch (By similarity).  
FT METAL 158 158 Calcium 1 (By similarity).  
FT METAL 168 168 Zinc 1 (By similarity).  
FT METAL 170 170 Zinc 1 (By similarity).  
FT METAL 175 175 Calcium 2 (By similarity).  
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 183 183 Zinc 1 (By similarity).  
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 194 194 Calcium 1 (By similarity).  
FT METAL 196 196 Zinc 1 (By similarity).

FT METAL 198 198 Calcium 2 (By similarity).  
FT METAL 201 201 Calcium 2 (By similarity).  
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).  
FT ACT\_SITE 219 219 By similarity.  
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).  
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).  
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT DISULFID 280 465 Probable.  
FT CARBOHYD 56 56 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 113 113 N-linked (GlcNAc...) (potential).  
SQ SEQUENCE 466 AA; 53277 MW; 8B9DB97576E76C90 CRC64;  
Query Match 67.1%; Score 196; DB 1; Length 466;  
Best Local Similarity 63.0%; Pred. No. 1.8e-16;  
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MQEFGGLKVTGKPDATLKVNMKQPCGVDPVAQFVLTEGPNRWEQTHLYRIEN 54  
Db 67 MQRFGLPETGKPDAAITIEINEKRCGVDPDGLLTPGSKWHTNLTIRIN 120  
RESULT 13  
MM10 HUMAN  
ID MM10 HUMAN STANDARD; PRT; 476 AA.  
AC P09238;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, last sequence update)  
DT 05-JUL-2004 (Rel. 44, last annotation update)  
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)  
DE (MMP-10) (Transin-2) (SL-2).  
GN Name=MMP10; Synonyms=STMY2;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=6833985; PubMed=2844164;  
RA Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.,  
RA Breathnach R.;  
RA "The collagenase gene family in humans consists of at least four  
RA members.";  
RL Biochem. J. 253:187-192(1988).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wallahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurnaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -|- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,

CC and V; weakly collagens III, IV, and V. Activates procollagenase.  
 CC -!- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on  
 CC collagen types III, IV and V is weak.  
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; X07820; CAA30679.1; -;  
 CC EMBL; BC002591; AA02591.1; -;  
 CC PIR; A28816; KCHUS2.  
 CC HSP; P08254; IG05.  
 CC MEROPS; M10.006; -;  
 CC Gene; HGNC:7156; MMP10.  
 CC MIM; 185260; -;  
 CC GO; GO:0005578; C:extracellular matrix; TAS.  
 CC GO; GO:0005615; C:extracellular space; TAS.  
 CC GO; GO:0004322; F:metalloendopeptidase activity; TAS.  
 CC GO; GO:0008270; F:zinc ion binding; TAS.  
 CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.  
 CC InterPro; IPR000585; Hemopexin.  
 CC InterPro; IPR006026; Peptidase M.  
 CC InterPro; IPR01818; Pept M10A\_M12B.  
 CC InterPro; IPR006025; Pept M Zn\_BS.  
 CC InterPro; IPR009070; Pept M Zn\_BS.  
 CC Pfam; PF00045; Hemopexin; 4.  
 CC Pfam; PF00413; Peptidase M10; 1.  
 CC Pfam; PF03933; Peptidase M10\_N; 1.  
 CC PRINTS; PR00138; MATRINX.  
 CC SMART; SM0120; HX; 4.  
 CC SMART; SM0235; ZNMc; 1.  
 CC PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 CC PROSITE; PS00024; HEMOPEXIN; 1.  
 CC PROSITE; PS00142; ZINC PROTEASE; 1.  
 CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;  
 KW Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 17 Probable.  
 FT PROPEP 18 98 Activation peptide.  
 FT CHAIN 99 476 Stromelysin-2.  
 FT DOMAIN 286 476 Hemopexin-like.  
 FT SITE 91 91 Cysteine switch (By similarity).  
 FT METAL 217 217 Zinc (catalytic) (By similarity).  
 FT ACT\_SITE 218 218 By similarity.  
 FT METAL 221 221 Zinc (catalytic) (By similarity).  
 FT METAL 227 227 Zinc (catalytic) (By similarity).  
 FT DISULFID 289 476 By similarity.  
 SQ SEQUENCE 476 AA; 54151 MW; 516DCDDFF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 1; Length 476;  
 Best Local Similarity 63.0%; Pred. No. 1.5e-15;  
 Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGPDATLKVWKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 DB 66 MQKFLGLEVTGKLDTDLEWVKRCGVPDVGHFSSFGMPKWKTKHLYRIEN 119

RESULT 14  
 ID AAP36110 PRELIMINARY; PRT; 476 AA.

AC AAP36110;  
 DT 02-MAR-2004 (TRENBLrel. 27, Created)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
 DE Matrix metalloproteinase 10 (Stromelysin 2).  
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
 CC Koundinya M., Raphael J., Morsira D., Kelley T., LaBaer J., Lin Y.,  
 CC Phelan M., Famer A.;  
 CC "Cloning of human full-length CDSs in BD Creator(TM) System Donor  
 CC RT vector";  
 CC RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 CC DR EMBL; BT007442; AAP36110.1; -;  
 CC SEQUENCE 476 AA; 54151 MW; 516DCDDFF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 2; Length 476;  
 Best Local Similarity 63.0%; Pred. No. 1.5e-15;  
 Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGPDATLKVWKQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 DB 66 MQKFLGLEVTGKLDTDLEWVKRCGVPDVGHFSSFGMPKWKTKHLYRIEN 119

RESULT 15  
 ID MM03 HUMAN STANDARD; PRT; 477 AA.

AC P08254;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)  
 DE (MMP-3) (Transin-1) (SL-1).  
 GN Name=MMP3; Synonyms=STWY1;  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.  
 CC RP MEDLINE=88198243; PubMed=3360803;  
 CC Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,  
 CC Kurkinen M.;  
 CC "The complete primary structure of human matrix metalloproteinase-3.  
 CC RT Identity with stromelysin.";  
 CC RL J. Biol. Chem. 263:6742-6745 (1988).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC RP TISSUE=Fibroblast;  
 CC MEDLINE=87156645; PubMed=3030290;  
 CC Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,  
 CC Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
 CC "Comparison of human stromelysin and collagenase by cloning and  
 CC sequence analysis.";  
 CC RL Biochem. J. 240:913-916 (1986).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC RP MEDLINE=88016164; PubMed=3477804;  
 CC Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,  
 CC Grant G.A., Bauer E.A., Goldberg G.I.;  
 CC "Human skin fibroblast stromelysin: structure, glycosylation,  
 CC RT substrate specificity, and differential expression in normal and  
 CC RT tumorigenic cells";  
 CC RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).  
 CC [4]  
 CC SEQUENCE FROM N.A.  
 CC RP Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
 CC Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
 CC Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
 CC Heller R., Davis R.W.;  
 CC Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 CC [5]  
 CC SEQUENCE FROM N.A., AND VARIANT GLU-45.  
 CC RP Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,

Nickerson D.A.;  
"SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-  
PHSC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";  
Submitted (AUG-2001) to the ENBL/GenBank/DBJ databases.  
[6]  
RN ZYMOGEN ACTIVATION.  
RP MEDLINE=90344802; PubMed=2383557;  
RX Nagase H., Englund J.J., Suzuki K., Salvesen G.;  
RT "Stepwise activation mechanisms of the precursor of matrix  
metalloproteinase 3 (stromelysin) by proteinases and (4-  
aminophenyl)mercuric acetate";  
RL Biochemistry 29:5783-5789(1990).  
RN  
RN STRUCTURE BY NMR OF CATALYTIC DOMAIN.  
RP MEDLINE=95384761; PubMed=7656014;  
RX Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,  
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,  
RA Johnson B.A.;  
RT "The NMR structure of the inhibited catalytic domain of human  
stromelysin-1";  
RL Nat. Struct. Biol. 1:111-118(1994).  
RN  
RN STRUCTURE BY NMR OF 100-267.  
RP MEDLINE=99043696; PubMed=9827994;  
RX Stockman B.J., Waldon D.J., Gates J.A., Scallill T.A.,  
RA Kloosterman D.A., Miazak S.A., Jacobsen E.J., Belonga K.L.,  
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,  
RA Ledbetter S.R., Kaytes P.S., Vogeli G., Marshall V.P., Petzold G.L.,  
RA Poorman R.A.;  
RT "Solution structures of stromelysin complexed to thiadiazole  
inhibitors";  
RL Protein Sci. 7:2281-2286(1998).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.  
RP MEDLINE=96117647; PubMed=8532233;  
RX Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,  
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,  
RA Hermes J.D., Springer J.P.;  
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic  
domain and of the C-truncated proenzyme";  
RL Protein Sci. 4:1966-1976(1995).  
RN  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.  
RP MEDLINE=96311273; PubMed=8740360;  
RX Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F.,  
RA Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F.,  
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;  
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin  
catalytic domain and its comparison with members of the zinc  
metalloproteinase superfamily";  
RL Structure 4:375-386(1996).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.  
RP MEDLINE=97236965; PubMed=9083493;  
RX Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L.,  
RA Girotra N.N., Kopka I.E., Lanza T.J., Levorse D.A., Maccoss M.,  
RA Owens K.A., Ponipom M.M., Simeone J.P., Harrison R.K.,  
RA Nedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,  
RA McDonnell J., Moore V.L., Olaszewski J.M., Saphos C., Visco D.M.,  
RA Shen F., Colletti A., Krier P.A., Hagmann W.K.;  
RT "Inhibition of stromelysin-1 (MMP-3) by P1'-biphenylylethyl  
carboxyalkyl dipeptides";  
RL J. Med. Chem. 40:1026-1040(1997).  
RN  
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH  
TIMP1.  
RP MEDLINE=97433330; PubMed=9288970;  
RX Gomis-Rueh P.-X., Maskos K., Betz M., Bergner A., Huber R.,  
RA Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,  
RA Bartunik H., Bode W.;  
RT "Mechanism of inhibition of the human matrix metalloproteinase  
stromelysin-1 by TIMP-1";  
RL Nature 389:77-81(1997).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.  
RP MEDLINE=9906562; PubMed=9792098;  
RX Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,  
RA Treped C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A.,  
RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.;  
RT "Structural characterizations of nonpeptidic thiadiazole inhibitors of  
matrix metalloproteinases reveal the basis for stromelysin  
selectivity";  
RL Protein Sci. 7:2118-2126(1998).  
RN  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.  
RP MEDLINE=20013067; PubMed=10543949;  
RX Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M.,  
RA Barnett B.L.;  
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A  
resolution: inhibitor-induced conformational changes";  
RL J. Mol. Biol. 293:545-557(1999).  
RN  
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.  
RP MEDLINE=99349695; PubMed=10422833;  
RX Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwein D.F., Johnson L.L.,  
RA Purchase C.F. II, White A.D., Dhanaraj V., Roth B.D., Johnson L.L.,  
RA Hupe D., Humblet C., Blundell T.L.;  
RT "X-ray structure of human stromelysin catalytic domain complexed with  
nonpeptide inhibitors: implications for inhibitor selectivity";  
RL Protein Sci. 8:1453-1462(1999).  
RN  
RN STRUCTURE BY NMR OF 100-272.  
RP MEDLINE=98434377; PubMed=9760240;  
RX Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.;  
RT "Solution structure of the catalytic domain of human stromelysin-1  
complexed to a potent, nonpeptidic inhibitor";  
RL Biochemistry 37:14048-14056(1998).  
RN  
RN FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,  
III, IV, and V; collagens III, IV, X, and IX, and cartilage  
proteoglycans. Activates procollagenase.  
RN CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'  
are hydrophobic residues.  
RN COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
RN SIMILARITY: Belongs to peptidase family M10A.  
RN SIMILARITY: Contains 1 hemopexin-like domain.  
RN  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
RN  
RN EMBL: X05232; CAA28859.1; -;  
DR EMBL: J03209; AAA36321.1; -;  
DR EMBL: U78045; AAB36942.1; -;  
DR EMBL: AF405705; AAK95247.1; -;  
DR FIC: A28156; KCHUS1.  
DR PDB: 1B3D; X-ray; A/B=100-272.  
DR PDB: 1B8Y; X-ray; A=100-266.  
DR PDB: 1B1W; X-ray; A/B=100-272.  
DR PDB: 1BM6; NMR; @=100-272.  
DR PDB: 1BQO; X-ray; A/B=100-272.  
DR PDB: 1C31; X-ray; A/B=100-272.  
DR PDB: 1C8T; X-ray; A/B=103-269.  
DR PDB: 1CAQ; X-ray; A=100-267.  
DR PDB: 1CIZ; X-ray; A=100-267.  
DR PDB: 1CQR; X-ray; A/B=100-272.  
DR PDB: 1D5J; X-ray; A/B=100-272.  
DR PDB: 1D7X; X-ray; A/B=100-272.  
DR PDB: 1D8F; X-ray; A/B=100-272.  
DR PDB: 1D8M; X-ray; A/B=100-272.  
DR PDB: 1G05; X-ray; A/B=100-272.  
DR PDB: 1G49; X-ray; A/B=100-272.  
DR PDB: 1G4K; X-ray; A/B=C=100-267.  
DR PDB: 1HFS; X-ray; @=105-264.

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DR PDB; 1HY7; X-ray; A/B=100-272.
DR PDB; 1M1W; Model; A=100-268.
DR PDB; 1OO9; NMR; A=100-267.
DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.
DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.
DR PDB; 1SLN; X-ray; @=18-272.

Query Match      64.7%  Score 189;  DB 1;  Length 477;
Best Local Similarity 63.0%  Pred. No. 1.5e-15;
Matches 34;  Conservative 9;  Mismatches 11;  Indels 0;  Gaps 0;

QY      1 MQEFGKLVTKGPDASTLKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
        67 MQRFGLGVTKLDSDTLEVYMKRRCGVPDVGHFRTFPGIPKWRKTHLYRIYN 120

Search completed: November 15, 2004, 14:06:38
Job time : 50.8462 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 50.4167 Seconds  
391.341 Million cell updates/sec

Title: US-10-032-376a-10  
Perfect score: 307  
Sequence: 1 MQRFFGLNVTKPNEETLDM.....LTPGNPKWNTLTIRINY 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1022821

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	6	ABP97132 Human mat
2	307	100.0	55	6	ABG76318 Human mat
3	307	100.0	55	8	ACQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AAB84610 Amino aci
6	307	100.0	467	4	AAE10416 Human mat
7	307	100.0	467	4	AAG65358 Human neu
8	307	100.0	467	6	ABO32581 Secreted
9	307	100.0	467	8	ADQ10212 Human pol
10	226	73.6	454	8	ADL93947 Human G-c
11	221	72.0	454	7	ADE16002 G-coupled
12	221	72.0	454	7	ADE16004 G-coupled
13	221	72.0	454	7	ADE16008 G-coupled
14	221	72.0	454	7	ADE16006 G-coupled
15	221	72.0	454	8	ADL93945 Human G-c
16	221	72.0	454	8	ADL93943 Human G-c
17	221	72.0	455	8	ADL93941 Human G-c
18	221	72.0	469	4	AAB84606 Amino aci
19	221	72.0	469	4	AAE10415 Human mat
20	221	72.0	469	6	ABU03466 Angiogene
21	221	72.0	469	6	ABR59543 Human can
22	221	72.0	469	6	ABR59542 Human can
23	221	72.0	469	6	ABR48148 Human bla
24	221	72.0	469	6	ABU56596 Lung canc
25	221	72.0	469	6	ABU56597 Lung canc

26	221	72.0	469	6	ABU07454	Abu07454 Protein d
27	221	72.0	469	6	ABE54454	Abp54454 Matrix me
28	221	72.0	469	7	ADB79176	Adb79176 Matrix me
29	221	72.0	469	7	ADE34550	Ades34550 Human ski
30	221	72.0	469	7	ADE16000	Adel6000 G-coupled
31	221	72.0	469	7	ADE16010	Adel6010 G-coupled
32	221	72.0	469	7	ADN39849	Adn39849 Cancer/an
33	221	72.0	469	7	ADN38694	Adn38694 Cancer/an
34	221	72.0	469	7	ADN38696	Adn38696 Cancer/an
35	221	72.0	469	7	ADN39850	Adn39850 Cancer/an
36	221	72.0	469	7	ADN95538	Adn95538 Human BEC
37	221	72.0	469	8	ADL93949	Adl93949 Human G-c
38	221	72.0	469	8	ADL93939	Adl93939 Human G-c
39	221	72.0	470	8	ADN07695	Adn07695 Human mat
40	221	72.0	490	7	AD207892	Ado7892 Novel pro
41	221	72.0	496	4	AAG75509	Aag75509 Human col
42	215	70.0	457	1	AAP93628	Aap93628 Sequence
43	215	70.0	469	1	AAP70611	Aap70611 Sequence
44	215	70.0	469	8	ADQ18359	Adq18359 Human sof
45	214	69.7	54	6	ABP97131	Abp97131 Human mat

ALIGNMENTS

RESULT 1  
ABP97132  
ID ABP97132 standard; peptide; 55 AA.  
XX  
AC ABP97132;  
XX

24-JUN-2003 (first entry)

Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant;  
vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;  
dermatological; metastatic; non-metastatic; vascularised; heart disease;  
non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
macular degeneration; diabetic retinopathy; cleavage region.

OS Homo sapiens.

XX WO2003018748-A2.

XX XX

PD 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

PR 21-DEC-2001; 2001US-00032376.

PR 21-MAY-2002; 2002US-00153185.

XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Weart IF;

XX WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (1) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 2

ABG76318  
 ID ABG76318 standard; protein; 55 AA.

AC ABG76318;

DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #10.

XX Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;  
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

PN WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

PI Quirk S, Malik S, Villanueva JM;

DR WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix

PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for

PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases  
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have  
 CC peptide sequences related to the cleavage regions of the proenzyme forms  
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular  
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin  
 CC development, treating wounds, preventing scarring, improving skin tone,  
 CC reducing wrinkling and for simulating the development of smooth, healthy  
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing  
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3

ADQ17093  
 ID ADQ17093 standard; peptide; 55 AA.

XX ADQ17093;

DT 23-SEP-2004 (first entry)

DE Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;  
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

PA (MALI/) MALIK S.

PA (QUIR/) QUIRK S.

PI Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds

PT comprises peptide having sequence related to matrix metalloproteinase

PT proenzyme.

XX Example 1; SEQ ID NO 10; 60pp; English.

XX The present invention provides peptides and compositions containing such  
 CC peptides that are useful as agents to maintain healthy skin and to  
 CC promote the condition of the skin. The invention is useful for increasing  
 CC the amount of fibronectin in tissue. The invention is also useful for  
 CC encouraging the maintenance and development of healthy skin, preventing  
 CC and treating wrinkles and for treating wounds. The invention acts as  
 CC vulnerary and dermatological agents. The present sequence is human matrix  
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in  
 CC the exemplification of the invention.

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MQRFFGLNVTGKPNBETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4

AAG65357  
 ID AAG65357 standard; protein; 444 AA.

XX AAG65357;

XX 30-NOV-2001 (first entry)

DE Human MMP-8alt polypeptide.  
XX  
KW MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;  
KW anti-arthritis; cytostatic; anti-Parkinsonian; neuroprotective;  
KW neutrotic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; human; splice variant.  
XX  
OS Homo sapiens.  
XX  
PN US1973-H.  
XX  
PD 03-JUL-2001.  
XX  
PF 22-OCT-1998; 98US-00178002.  
XX  
PR 22-OCT-1998; 98US-00178002.  
XX  
PA (NOVS ) NOVARTIS AG.  
XX  
PI Hu S;  
XX  
WPI: 2001-431511/46.  
DR N-PSDB; AAH47515.  
XX  
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents  
PT and materials for discovering treatments and diagnostics to human  
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.  
XX  
PS Claim 11; Col 25-30; 25pp; English.  
XX  
CC The invention relates to human MMP-8alt polypeptide and polynucleotides.  
CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)  
CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant  
CC methodology. The polynucleotides and polypeptides may be used as research  
CC reagents and materials for the discovery of treatments and diagnostics to  
CC human disease, and as targets for identifying modulators. Inhibitors of  
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat  
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases  
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's  
CC disease and Huntington's disease. The present sequence represents the  
CC human MMP-8alt polypeptide  
XX  
SQ Sequence 444 AA;  
Query Match 100.0%; Score 307; DB 4; Length 444;  
Best Local Similarity 100.0%; Pred. No. 4.4e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MORFFGLNVTGKPNETLDMKKPCGVPDGGFMTGPNKWERNTLYIRNY 55  
DB 43 MORFFGLNVTGKPNETLDMKKPCGVPDGGFMTGPNKWERNTLYIRNY 97  
RESULT 5  
AAB84610  
ID AAB84610 standard; protein; 467 AA.  
XX  
AC AAB84610;  
XX  
DT 05-SEP-2001 (first entry)  
XX  
DE Amino acid sequence of matrix metalloproteinase-8.  
XX  
KW Growth factor; protein inhibitor; protease; damaged tissue;  
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;  
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;  
KW vascular endothelial growth factor; urokinase plasminogen activator;  
KW dermal ulcer; wound.  
XX  
OS Homo sapiens.

XX WO200149309-A2.  
PN  
XX 12-JUL-2001.  
PD  
XX 21-DEC-2000; 2000WO-IB001935.  
PF  
XX 29-DEC-1999; 99GB-00030768.  
PR  
XX (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX  
PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;  
XX  
WPI: 2001-418351/44.  
DR N-PSDB; AAH28225.  
XX  
XX Composition for the treatment of damaged tissue i.e. chronic wounds and  
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth  
PT factor.  
XX  
PS Disclosure; Page 555; 572pp; English.  
XX  
CC The specification describes a pharmaceutical composition, comprising a  
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent  
CC inhibits the action of at least one specific adverse protein, i.e. a  
CC protease, that is upregulated in a damaged tissue such as a wound  
CC environment. Growth factors which are included in the composition of the  
CC invention are platelet-derived growth factor (PDGF), fibroblast growth  
CC factor (FGF), connective tissue derived growth factor (CTGF),  
CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta  
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),  
CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),  
CC and chrysalin. Inhibitors which are included in the composition of the  
CC invention include inhibitors of urokinase-type plasminogen activator  
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for  
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.  
CC The present sequence represents a human MMP-8, and is used to produce the  
CC composition of the invention  
XX  
SQ Sequence 467 AA;  
Query Match 100.0%; Score 307; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MORFFGLNVTGKPNETLDMKKPCGVPDGGFMTGPNKWERNTLYIRNY 55  
DB 66 MORFFGLNVTGKPNETLDMKKPCGVPDGGFMTGPNKWERNTLYIRNY 120  
RESULT 6  
AAE10416  
ID AAE10416 standard; protein; 467 AA.  
XX  
AC AAE10416;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Human matrix metalloproteinase-8 (MMP-8) protein.  
XX  
KW Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;  
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
XX 1..20  
FT Peptide /label= Signal\_peptide  
XX 21..467  
FT Protein /label= Mature\_MMP\_8\_protein  
XX 89..95  
FT Domain /label= Cysteine\_switch\_domain  
XX



PA (FRASER) FRASER C C.  
 PA (BARN) BARNES T M.  
 PA (SHAR) SHARP J D.  
 PA (KIRST) KIRST S J.  
 PA (MYER) MYERS P S.  
 PA (LEIB) LEIBY K R.  
 PA (HOLT) HOLTZMAN D A.  
 PA (MCCA) MCCARTHY S A.  
 PA (WRIG) WRIGHTON N.  
 PA (MACK) MACKAY C R.  
 PA (GOOD) GOODEARL A D J.  
 XX  
 XX Fraser CC, Barnes TM, Sharp JD, KIRST SJ, Myers PS, Leiby KR;  
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
 XX  
 XX WPI; 2003-456290/43.  
 DR N-PSDB; ACD66741.  
 XX  
 XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,  
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in  
 PT forensic biology.  
 XX  
 XX Disclosure; Fig 15V-15W; 482pp; English.  
 PS  
 PS The invention relates to secreted polypeptide-related proteins and  
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The  
 CC nucleic acids, proteins and antibodies specific to the proteins are  
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and  
 CC prophylactic and therapeutic methods. The sequences are used in  
 CC diagnosing, preventing or treating proliferative disorders (e.g.  
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders  
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood  
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
 CC acids may also be used in chromosome mapping, tissue typing and forensic  
 CC biology, and as surrogate markers. This sequence represents a secreted  
 CC polypeptide-related protein of the invention. Note: The sequence data for  
 CC this patent was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 XX Sequence 467 AA;  
 SQ  
 Query Match 100.0%; Score 307; DB 6; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
 Db 56 MORFFGLNVTGKPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120  
 RESULT 9  
 ID ADQ10212  
 AC ADQ10212 standard; protein; 467 AA.  
 XX ADQ10212;  
 XX  
 XX 09-SEP-2004 (first entry)  
 DT  
 DE Human polypeptide #75.  
 XX  
 XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;  
 KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;  
 KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;  
 KW arteriosclerosis; hypertension; bacterial infection; psoriasis;  
 KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;  
 KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;  
 KW goiter; infertility; endometriosis; muscular disorder.

OS Homo sapiens.  
 XX  
 XX US2004121396-A1.  
 PN  
 XX 24-JUN-2004.  
 PD  
 XX  
 XX 19-DEC-2003; 2003US-00741790.  
 PF  
 XX 14-JUN-1999; 99US-00333159.  
 PR 29-JUN-1999; 99US-00342364.  
 PR 10-SEP-1999; 99US-00393996.  
 PR 19-OCT-1999; 99US-00420707.  
 PR 07-JAN-2000; 2000US-00479249.  
 PR 27-APR-2000; 2000US-00559497.  
 PR 24-MAY-2000; 2000US-00578063.  
 PR 16-JUN-2000; 2000US-00596194.  
 PR 23-JUN-2000; 2000US-00602871.  
 PR 30-JUN-2000; 2000US-00608452.  
 PR 12-JAN-2001; 2001US-00759130.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 PI Fraser CC, Barnes TM, Sharp JD, KIRST SJ, Myers PS, Leiby KR;  
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
 XX  
 XX WPI; 2004-479675/45.  
 DR  
 XX  
 XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and  
 PT treating cancer, constipation, hemorrhoids, cystic fibrosis, and  
 PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,  
 PT tuberculosis, malaria, goiter, infertility.  
 XX  
 XX Disclosure; SEQ ID NO 176; 483pp; English.  
 PS  
 PS The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The invention also relates to a host cell containing a  
 CC polynucleotide of the invention, an antibody which selectively binds to a  
 CC polypeptide of the invention, a method of detecting the presence of a  
 CC polypeptide in a sample, a method of identifying a compound which binds  
 CC with a polypeptide, and a method of modulating the activity of a  
 CC polypeptide. The polynucleotides, polypeptides and compositions are  
 CC useful for diagnosing, preventing and/or treating cancer, obesity,  
 CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host  
 CC reactions, allergic reactions, cystic fibrosis, hypogonadism,  
 CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,  
 CC hypertension, bacterial infections, psoriasis, diabetes mellitus,  
 CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's  
 CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,  
 CC infertility, endometriosis, wounds and muscular disorders. This sequence  
 CC represents a human polypeptide of the invention. Note: The sequence data  
 CC for this patent did not form part of the printed specification but was  
 CC obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 XX Sequence 467 AA;  
 SQ  
 Query Match 100.0%; Score 307; DB 8; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MORFFGLNVTGKPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
 Db 66 MORFFGLNVTGKPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120  
 RESULT 10  
 ID ADL93947  
 XX ADL93947 standard; protein; 454 AA.  
 XX  
 XX ADL93947;  
 XX  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX

DE Human G-coupled protein receptor-related protein #19.

XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;

KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;

KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;

KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

KW Crohn's disease; G-coupled protein receptor; metabolic disorder;

XX neurodegenerative disorder; receptor.

OS Homo sapiens.

XX US2004006205-A1.

PN 08-JAN-2004.

XX 02-APR-2002; 2002US-00115479.

XX 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 10-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283687P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285609P.

PR 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.

PR 24-APR-2001; 2001US-0286068P.

PR 27-APR-2001; 2001US-0287213P.

PR 30-MAY-2001; 2001US-0288509P.

PR 31-MAY-2001; 2001US-0294495P.

PR 31-MAY-2001; 2001US-0294801P.

PR 31-JUL-2001; 2001US-0309216P.

PR 25-SEP-2001; 2001US-0324775P.

PR 28-NOV-2001; 2001US-0333900P.

XX (LILL/) LI L.

PA (GERL/) GERLACH V.

PA (LIUX/) LIU X.

PA (MILL/) MILLER C E.

PA (SPYT/) SPYTER K A.

PA (ZERR/) ZERHUSEN B D.

PA (PENA/) PENA C E A.

PA (SHEN/) SHENOY S G.

PA (ZHON/) ZHONG H.

PA (SMIT/) SMITHSON J.

PA (CASM/) CASMAN S J.

PA (BOLD/) BOLDOG F L.

PA (VOSS/) VOSS E Z.

PA (VERN/) VERNET C A.

PA (MACD/) MACDOUGALL J R.

PA (RASP/) RASTELLI L.

PA (ANDE/) ANDERSON D W.

PA (ZHON/) ZHONG M.

PA (MEZE/) MEZES P S.

PA (FURT/) FURTAK K.

PA (PATT/) PATTURAJAN M.

PA (BURG/) BURGESS C E.

PA (MALV/) MALYANKAR U M.

PA (SHIM/) SHIMKETS R A.

PA (TAUP/) TAUPIER R J.

PA (EDIN/) EDINGER S.

PA (MAZU/) MAZUR A.

PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;

PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;

XX WPI; 2004-224146/21.

DR N-PSDB; ADL93946.

XX New G-coupled protein-receptor related polypeptides, for preventing

PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,

PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,

PT scleroderma or obesity.

XX Claim 1; Page 69; 220pp; English.

XX The invention relates to isolated human G-coupled protein receptor-

CC related polypeptides and polynucleotides. The proteins are useful for

CC preventing, treating or ameliorating medical disorders by protein or gene

CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,

CC congenital heart defects, aortic stenosis, atrial septal defect,

CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,

CC subaortic stenosis, ventricular septal defect, valve diseases, tuberculous

CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,

CC congenital adrenal hyperplasia, prostate cancer, neoplasm,

CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,

CC hypercoagulation, idiopathic thrombocytopenic purpura,

CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,

CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They

CC are also useful as diagnostic or research tools. The present sequence

CC represents a human G-coupled protein receptor-related protein of the

CC invention.

XX Sequence 454 AA;

SQ Query Match 73.6%; Score 226; DB 8; Length 454;

Best Local Similarity 72.7%; Pred. No. 6e-22;

Matches 40; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNETLMKMKPCGVPDSCGEMLTGCPKWTNLTIRNY 55

DB 50 MQEFFGLKVTGKPDATLTKMKQPCGVPDVAQVLTGCPKWTNLTIRNY 104

RESULT 11

ADE16002

ID ADE16002 standard; protein; 454 AA.

XX ADE16002;

XX 29-JAN-2004 (first entry)

XX G-coupled protein receptor related polypeptide, SEQ ID No 32.

XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;

KW virucide; fungicide; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;

KW cell differentiation; cell proliferation; hematopoiesis; wound healing;

KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

XX preventive medicine; pharmacogenomics; human.

XX Homo sapiens.

XX WO200283841-A2.

XX 24-OCT-2002.

XX 03-APR-2002; 2002WO-US010713.

XX 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 10-APR-2001; 2001US-0281906P.

PR 13-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

13-APR-2001; 2001US-0283678P.  
 13-APR-2001; 2001US-0283687P.  
 13-APR-2001; 2001US-0283710P.  
 17-APR-2001; 2001US-0284234P.  
 19-APR-2001; 2001US-0285325P.  
 20-APR-2001; 2001US-0285609P.  
 23-APR-2001; 2001US-0285748P.  
 23-APR-2001; 2001US-0285909P.  
 24-APR-2001; 2001US-0286068P.  
 27-APR-2001; 2001US-0287213P.  
 30-MAY-2001; 2001US-0288509P.  
 30-MAY-2001; 2001US-0294495P.  
 31-MAY-2001; 2001US-0294801P.  
 31-JUL-2001; 2001US-0309216P.  
 25-SEP-2001; 2001US-0324775P.  
 28-NOV-2001; 2001US-0333900P.  
 02-APR-2002; 2002US-00115479.  
 (CURA-) CURAGEN CORP.  
 Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
 Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DM;  
 Shong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UV;  
 Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
 WPI: 2003-057574/06.  
 N-PSDB; ADE16001.  
 New isolated NOVX polypeptides and polynucleotides, useful for  
 preventing, diagnosing or treating NOVX-associated disorders e.g.  
 diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 Alzheimer's disease, infections.  
 Claim 1; SEQ ID NO 32; 320pp; English.  
 The invention relates to a novel isolated G-coupled protein receptor  
 related polypeptides. The novel polypeptide comprise any of the 22 fully  
 defined sequences of 87-1780 amino acids, given in the specification;  
 their mature forms; and possible variants. The novel polypeptides have  
 the following activities: antidiabetic, anorectic, antibacterial,  
 virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
 antiParkinsonian, haemostatic, and antilipemic. The G-coupled protein  
 receptor related polypeptides are useful in a method of treating or  
 preventing in a human, a pathology associated with the G-coupled protein  
 receptor related polypeptides. The polypeptides are useful in the  
 manufacture of a medicament for treating a syndrome associated with a  
 human disease, preferably a NOVX-associated disorder. The novel  
 polypeptides are useful for treating, preventing or diagnosing diseases,  
 such as metabolic disorders, diabetes, obesity, infectious diseases,  
 anorexia, cancer-associated diseases, neurodegenerative disorders,  
 Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 disorders, and various dyslipidaemias, metabolic disturbances associated  
 with obesity, metabolic X syndrome and wasting disorders associated with  
 chronic diseases and various cancers. The nucleic acids and polypeptides  
 may also be used as targets for the identification of small molecules  
 that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 therapy, in generation of antibodies that bind immunospecifically to NOVX  
 substances for use in therapeutic or diagnostic methods, The nucleic  
 acids are further used as hybridization probes, in chromosome mapping,  
 tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 represents one of the novel G-coupled protein receptor related  
 polypeptides of the invention.  
 Sequence 454 AA;  
 Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0  
 1 MQRFGLVNTGKPNHEITLDMKKPCGVPDGGFMLTGPNKWRTNLTIRNY 55

CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaeic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.  
 XX  
 XX Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNKWTNLTIRNY 55  
 DB 50 MQEFGKLVTKGPDATLTKWKQPRCGVPSDVAQFVLTEGPRWEQTHLYRIENY 104

RESULT 13  
 ADE16008  
 ID ADE16008 standard; protein; 454 AA.  
 XX ADE16008;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX G-coupled protein receptor related polypeptide, SEQ ID NO 38.  
 DE  
 XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
 KW virucide; fungicide; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; haemostatic; antilipaeic; neurogenesis;  
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
 KW preventive medicine; pharmacogenomics; human.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200283841-A2.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 03-APR-2002; 2002WO-US010713.  
 XX  
 XX 03-APR-2001; 2001US-0281136P.  
 XX  
 XX 05-APR-2001; 2001US-0281863P.  
 XX  
 XX 10-APR-2001; 2001US-0281906P.  
 XX  
 XX 13-APR-2001; 2001US-0282394P.  
 XX  
 XX 13-APR-2001; 2001US-0283657P.  
 XX  
 XX 13-APR-2001; 2001US-0283678P.  
 XX  
 XX 13-APR-2001; 2001US-0283687P.  
 XX  
 XX 17-APR-2001; 2001US-0283710P.  
 XX  
 XX 19-APR-2001; 2001US-0284234P.  
 XX  
 XX 20-APR-2001; 2001US-0285325P.  
 XX  
 XX 23-APR-2001; 2001US-0285609P.  
 XX  
 XX 23-APR-2001; 2001US-0285746P.

PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.  
 PR 27-APR-2001; 2001US-0287213P.  
 PR 03-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 PR 02-APR-2002; 2002US-00115479.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FI;  
 PI Voss EA, Vernet CAM, MacDougall JR, Rastelli L, Anderson DW;  
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shimkets RA, Taupier RV, Edinger SR, Mazur A;  
 XX  
 XX WPI; 2003-067574/06.  
 DR N-PSDB; ADE16007.  
 XX  
 XX New isolated NOX polypeptides and polynucleotides, useful for  
 XX preventing diagnosing or treating NOX-associated disorders e.g.  
 XX diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 XX Alzheimer's disease, infections.  
 XX  
 XX Claim 1; SEQ ID NO 38; 320pp; English.

PS The invention relates to a novel isolated G-coupled protein receptor  
 XX related polypeptides. The novel polypeptide comprise any of the 22 fully  
 CC defined sequences of 87-1780 amino acids, given in the specification;  
 CC their mature forms; and possible variants. The novel polypeptides have  
 CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaeic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.

Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSDGGFMLTPGNKWTNLTIRNY 55  
 DB 50 MQEFGKLVTKGPDATLTKWKQPRCGVPSDVAQFVLTEGPRWEQTHLYRIENY 104

RESULT 14  
 ADE16006  
 ID ADE16006 standard; protein; 454 AA.  
 XX



AC ADE16006;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE G-coupled protein receptor related polypeptide, SEQ ID NO 36.  
XX  
DE G-coupled protein receptor; anorectic; antidiabetic; virucide; fungicide; cytostatic; neurotropic; antiparkinsonian; haemostatic; antilipemic; neurogenesis;  
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
KW preventive medicine; pharmacogenomics; human.  
XX  
XX Homo sapiens.  
OS  
XX WO200283841-A2.  
PN  
XX  
XX 24-OCT-2002.  
PD  
XX  
XX 03-APR-2002; 2002WO-US010713.  
XX  
XX 03-APR-2001; 2001US-0281136P.  
PR  
XX 05-APR-2001; 2001US-0281863P.  
PR  
XX 05-APR-2001; 2001US-0281906P.  
PR  
XX 10-APR-2001; 2001US-0282934P.  
PR  
XX 13-APR-2001; 2001US-0283657P.  
PR  
XX 13-APR-2001; 2001US-0283678P.  
PR  
XX 13-APR-2001; 2001US-0283687P.  
PR  
XX 13-APR-2001; 2001US-0283710P.  
PR  
XX 17-APR-2001; 2001US-0284234P.  
PR  
XX 19-APR-2001; 2001US-0285325P.  
PR  
XX 20-APR-2001; 2001US-0285609P.  
PR  
XX 23-APR-2001; 2001US-0285748P.  
PR  
XX 23-APR-2001; 2001US-0285890P.  
PR  
XX 24-APR-2001; 2001US-0286068P.  
PR  
XX 27-APR-2001; 2001US-0287213P.  
PR  
XX 03-MAY-2001; 2001US-0288509P.  
PR  
XX 30-MAY-2001; 2001US-0294495P.  
PR  
XX 31-JUL-2001; 2001US-0294801P.  
PR  
XX 31-JUL-2001; 2001US-0309218P.  
PR  
XX 25-SEP-2001; 2001US-0324775P.  
PR  
XX 28-NOV-2001; 2001US-0333900P.  
PR  
XX 02-APR-2002; 2002US-00115479.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI Pena CRA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CB, Malyankar UM;  
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX  
XX WPI; 2003-067574/06.  
DR  
XX N-PSDB; ADE16005.  
DR  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX  
XX Claim 1; SEQ ID NO 36; 320pp; English.  
PS  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a

CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
XX Sequence 454 AA;  
SQ

Query Match 72.0%; Score 221; DB 7; Length 454;  
Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 MQRPFLNVTGKNEETLDMKKXPRGVPDSGGFMTGPNKWERNTLYRIINY 55  
Db 50 MQEFGKLVTKGPDATLTKVMKQPRGVPDVAQFVLTEGNPRWEQTHLYRIENY 104

RESULT 15  
ADL93945  
ID ADL93945 standard; protein; 454 AA.  
XX  
XX ADL93945;  
AC  
XX 20-MAY-2004 (first entry)  
DT  
XX  
DE Human G-coupled protein receptor-related protein #18.  
XX  
XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;  
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;  
KW valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;  
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;  
KW hemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;  
KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;  
KW Crohn's disease; G-coupled protein receptor; metabolic disorder;  
KW neurodegenerative disorder; receptor.  
XX  
XX Homo sapiens.  
OS  
XX US2004006205-A1.  
PN  
XX  
XX 08-JAN-2004.  
PD  
XX  
XX 02-APR-2002; 2002US-00115479.  
PF  
XX  
XX 03-APR-2001; 2001US-0281136P.  
PR  
XX 05-APR-2001; 2001US-0281863P.  
PR  
XX 05-APR-2001; 2001US-0281906P.  
PR  
XX 10-APR-2001; 2001US-0282934P.  
PR  
XX 13-APR-2001; 2001US-0283657P.  
PR  
XX 13-APR-2001; 2001US-0283678P.  
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XX 13-APR-2001; 2001US-0283687P.  
PR  
XX 13-APR-2001; 2001US-0283710P.  
PR  
XX 17-APR-2001; 2001US-0284234P.  
PR  
XX 19-APR-2001; 2001US-0285325P.  
PR  
XX 20-APR-2001; 2001US-0285609P.  
PR  
XX 23-APR-2001; 2001US-0285748P.  
PR  
XX 23-APR-2001; 2001US-0285890P.  
PR  
XX 24-APR-2001; 2001US-0286068P.  
PR



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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 14.8077 Seconds  
(without alignments)  
246.324 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKPNETLDM.....LTPGNPKWERNLTIRIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 205538

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/aaa/5A\_COMB.pep:\*\n2: /cgn2\_6/ptodata/1/aaa/5B\_COMB.pep:\*\n3: /cgn2\_6/ptodata/1/aaa/6A\_COMB.pep:\*\n4: /cgn2\_6/ptodata/1/aaa/6B\_COMB.pep:\*\n5: /cgn2\_6/ptodata/1/aaa/PCTUS\_COMB.pep:\*\n6: /cgn2\_6/ptodata/1/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	444	1	US-09-178-002-2
2	307	100.0	466	3	US-08-704-711A-17
3	307	100.0	466	3	US-09-521-220-17
4	307	100.0	467	1	US-09-178-002-4
5	307	100.0	467	3	US-09-391-104-24
6	307	100.0	468	3	US-08-448-489-13
7	221	72.0	469	3	US-08-704-711A-16
8	221	72.0	469	3	US-08-448-489-12
9	221	72.0	469	3	US-09-521-220-16
10	221	72.0	469	3	US-09-391-104-23
11	196	63.8	477	3	US-08-704-711A-20
12	196	63.8	477	3	US-08-448-489-15
13	196	63.8	477	3	US-08-281-313-1
14	196	63.8	477	3	US-09-521-220-20
15	196	63.8	477	3	US-09-391-104-21
16	195	63.5	476	3	US-08-704-711A-21
17	195	63.5	476	3	US-08-448-489-14
18	195	63.5	476	3	US-09-521-220-21
19	195	63.5	476	3	US-09-391-104-22
20	188	61.2	471	3	US-09-391-104-25
21	179	58.3	471	4	US-08-994-689C-1
22	172	56.0	471	4	US-08-994-689C-21
23	164	53.4	513	4	US-10-140-002-192
24	164	53.4	513	4	US-09-862-631-4
25	160	52.1	264	3	US-09-009-156-6
26	160	52.1	264	3	US-09-372-154-6
27	160	52.1	267	3	US-08-448-489-18

28 160 52.1 267 3 US-09-391-104-27 Sequence 27, Appli  
29 160 52.1 271 3 US-08-896-062-2 Sequence 2, Appli  
30 160 52.1 470 3 US-08-088-392-2 Sequence 2, Appli  
31 160 52.1 470 3 US-08-396-988-2 Sequence 2, Appli  
32 160 52.1 470 3 US-09-391-104-26 Sequence 26, Appli  
33 159 51.8 135 4 US-09-513-999C-4163 Sequence 4163, Ap  
34 153 49.8 631 3 US-08-448-489-17 Sequence 17, Appli  
35 153 49.8 660 3 US-08-704-711A-18 Sequence 18, Appli  
36 153 49.8 660 3 US-09-521-220-19 Sequence 19, Appli  
37 153 49.8 660 3 US-09-391-104-19 Sequence 19, Appli  
38 153 49.8 660 4 US-09-917-254-89 Sequence 89, Appli  
39 143.5 46.7 604 3 US-09-391-104-30 Sequence 30, Appli  
40 143.5 46.7 607 3 US-09-000-041A-2 Sequence 2, Appli  
41 143.5 46.7 607 3 US-09-211-704A-10 Sequence 10, Appli  
42 143.5 46.7 607 4 US-09-734-002-2 Sequence 2, Appli  
43 142 46.3 136 4 US-09-513-999C-4639 Sequence 4639, Ap  
44 138 45.0 462 3 US-08-068-392-3 Sequence 3, Appli  
45 138 45.0 462 3 US-08-396-988-3 Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-178-002-2  
; Sequence 2, Application US/09178002  
; Patent No. H001973  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Shou-Ih  
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
; FILE REFERENCE: CGC 2048  
; CURRENT APPLICATION NUMBER: US/09/178,002  
; CURRENT FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-32;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNETLDMKKPCGVPDGGFMLTPGNPKWERNLTIRIRNY 55  
Db 43 MQRFFGLNVTGKPNETLDMKKPCGVPDGGFMLTPGNPKWERNLTIRIRNY 97

RESULT 2  
US-08-704-711A-17  
; Sequence 17, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 466 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-17

Query Match 100.0%; Score 307; DB 3; Length 466;  
Best Local Similarity 100.0%; Pred. No. 5.5e-32;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55  
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

## RESULT 3

US-09-521-220-17  
Sequence 17, Application US/09521220  
Patent No. 639348  
GENERAL INFORMATION:  
APPLICANT: WILL, Horst  
HINZMANN, Bernd  
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
METALLOPROTEASES, THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/521,220  
FILING DATE: 08-Mar-2000  
CLASSIFICATION: <Unknown>  
21-OCT-1994  
17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/704,711  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:

NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 466 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-521-220-17

Query Match 100.0%; Score 307; DB 3; Length 466;  
Best Local Similarity 100.0%; Pred. No. 5.5e-32;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55  
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

## RESULT 4

US-09-178-002-4  
Sequence 4, Application US/09178002  
Patent No. H001973  
GENERAL INFORMATION:  
APPLICANT: Hu, Shou-Ih  
TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
FILE REFERENCE: CGC 2048  
CURRENT APPLICATION NUMBER: US/09/178,002  
CURRENT FILING DATE: 1998-10-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;  
Best Local Similarity 100.0%; Pred. No. 5.6e-32;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55  
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

## RESULT 5

US-09-391-104-24  
Sequence 24, Application US/09391104  
Patent No. 639371  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
FALDUTO, Michael T.  
APPLICANT: Magnuson, Scott R.  
APPLICANT: Morgan, Douglas W.  
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.  
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
TITLE OF INVENTION: OP USING SAME  
FILE REFERENCE: 6073.US.PI  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07  
PRIOR APPLICATION NUMBER: US 08/814,394  
PRIOR FILING DATE: 1997-03-11  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 467

; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-391-104-24  
 Query Match 100.0%; Score 307; DB 3; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-32; Indels 0; Gaps 0;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRINY 55  
 Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRINY 120  
 RESULT 6  
 US-08-448-489-13  
 ; Sequence 13, Application US/08448489  
 ; Patent No. 6184022  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SEIKI, Motoharu  
 ; APPLICANT: SATO, Hiroshi  
 ; APPLICANT: SHINAGAWA, Akira  
 ; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
 ; FILE REFERENCE: 55-290P  
 ; CURRENT APPLICATION NUMBER: US/08/448,489  
 ; CURRENT FILING DATE: 1995-06-07  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 13  
 ; LENGTH: 468  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: X = UNKNOWN  
 ; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
 ; OTHER INFORMATION: Matrix Metalloproteinase Family  
 US-08-448-489-13  
 Query Match 100.0%; Score 307; DB 3; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-32; Indels 0; Gaps 0;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRINY 55  
 Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGNPKWERTNLTIRINY 120  
 RESULT 7  
 US-08-704-711A-16  
 ; Sequence 16, Application US/08704711A  
 ; Patent No. 614159  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILL, Horst  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/704,711A  
 ; FILING DATE: 20-NOV-1996  
 ; CLASSIFICATION: 435

TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
METALLOPROTEASES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/521,220  
FILING DATE: 08-Mar-2000  
CLASSIFICATION: <Unknown>  
21-OCT-1994  
17-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/704,711  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
15-09-521-220-16

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Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

      1  MQRFFGLNVTKGPKNEETLDMWKPRGCVDPDSGGFMLTGNPKWERTNLTYSIRNY 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      67  MQEFFGLKVTGKPAETLKWKQPRGCVDPDAQFVLTEGPRWEQTHLTYSIRNY 121
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-391-104-23
; Sequence 23, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falcuto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 23
;
; LENGTH: 469
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-09-391-104-23

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Query Match	72.0%	Score 21;	DB 3;	Length 469;
Best Local Similarity	70.9%	Match No. 1.1e-20;		
Matches 39;	Conservative	7;	Mismatches 20;	Indels 0; Gaps
QY	1	MQRFGLVNTGKNEETLDMKKPKRGVDPDSCGFVLTGPNKRWERTNLTYYRNY	55	
DB	67	MQRFGLVNTGKNEETLDMKKPKRGVDPDSCGFVLTGPNKRWERTNLTYYRNY	121	

RESULT 11  
 US-08-704-711A-20  
 ; Sequence 20, Application US/08704711A  
 ; Patent No. 6114159  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILL, Horst  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K-Street, N.W., Suite 500  
 ; City: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA

ZIP: 20007-S109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-20

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Query Match      63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.le-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps
QY      1  MQRFFGLNVATGKPEEETIDMMKPRCGVPDGGFMTLPNGPKWERNLNLYRYNY 55
Db      67  MOKFVGLVETGKLDSDILEVNRKPRCGVPDVGHFRTFFPGIPKWKTHLYRYNY 12

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RESULT 12  
US-08-448-489-15  
Sequence 15, Application US/08448489  
Patent No. 6184022  
GENERAL INFORMATION:  
APPLICANT: SEIKI, Motoharu  
APPLICANT: SATO, Hiroshi  
APPLICANT: SHINAGAWA, Akira  
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
FILE REFERENCE: 55-290P  
CURRENT APPLICATION NUMBER: US/08/448,489  
CURRENT FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15  
LENGTH: 477  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Known Member of  
OTHER INFORMATION: Matrix Metalloproteinase family  
US-08-448-489-15  
Query Match 63.8%; Score 196; DB 3; Length 477;  
Best Local Similarity 63.6%; Pred. No. 2.1e-17;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MQRFGLNVTGKPNBETLDMKKPCGVPDSCGFMLTPGNPKWERTNLTIRNY 55  
Db 67 MQKFLGLEVTGKLDSDTLEWVRKPCGVPDVGHFRTFFGIPKWRKTHLTIRVNY 121  
RESULT 13  
US-08-281-313-1  
Sequence 9, Application US/09368169  
Patent No. 6284511  
GENERAL INFORMATION:  
APPLICANT: Tetsuya INAKA et al.  
TITLE OF INVENTION: HEAT-STABLE PROLYNDOPEPTIDASE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/368,169  
FILING DATE: August 5, 1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/750,816  
FILING DATE: January 8, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: 99-0868/LC(WMC)49  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acid residues  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
ORIGINAL SOURCE:  
ORGANISM: Flavobacterium meningosepticum  
ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Ala V  
ORGANISM: 1  
Sequence 1, Application US/08281313  
Patent No. 6284513  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhuang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
APPLICANT: Baragi, Vijaykumar  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Stromelysin Catalytic Domain Protein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/281,313  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,705  
FILING DATE: 03-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Tinney, Francis J.  
REGISTRATION/DOCKET NUMBER: 4415-01-FUT  
REFERENCE/DOCKET NUMBER: 4415-01-FUT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 100.273  
OTHER INFORMATION: /note= "Mature stromelysin  
OTHER INFORMATION: catalytic domain protein"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1.17  
OTHER INFORMATION: /note= "Signal peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 18.99  
OTHER INFORMATION: /note= "Propeptide"  
US-08-281-313-1  
Query Match 63.8%; Score 196; DB 3; Length 477;  
Best Local Similarity 63.6%; Pred. No. 2.1e-17;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MQRFGLNVTGKPNBETLDMKKPCGVPDSCGFMLTPGNPKWERTNLTIRNY 55  
Db 67 MQKFLGLEVTGKLDSDTLEWVRKPCGVPDVGHFRTFFGIPKWRKTHLTIRVNY 121

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RESULT 14
US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20
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Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFFGLNVTGKPNETLDMKKKPCGVPDSCGFMLTGPNPKWERTNLTIRNY 55
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 67 MQKFLGLEVTGKLDSDTLEVMRPRCGVPDVGHFRTFGIPKWKTHLTIRVNY 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 15, 2004, 14:08:08
Job time : 15.8077 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:06:45 ; Search time 142.436 Seconds  
(without alignments)  
136.623 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307  
Sequence: 1 MORFFGLNVTGKPNBEETLDM.....LTPGNPKWERTNLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1077212

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pap.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pap.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pap.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pap.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pap.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	55	14	US-10-219-329-10
2	307	100.0	55	14	US-10-153-185-10
3	307	100.0	55	14	US-10-219-561-10
4	307	100.0	55	16	US-10-032-376A-10
5	307	100.0	55	16	US-10-335-207-10
6	307	100.0	467	9	US-09-391-104-24
7	307	100.0	467	9	US-09-801-196-20
8	307	100.0	467	10	US-09-759-130B-176
9	307	100.0	467	14	US-10-131-985-31
10	307	100.0	467	16	US-10-741-790-176
11	221	72.0	454	15	US-10-115-479-32
12	221	72.0	454	15	US-10-115-479-34
13	221	72.0	454	15	US-10-115-479-36

14	221	72.0	454	15	US-10-115-479-38	Sequence 38, Appl
15	221	72.0	469	9	US-09-391-104-23	Sequence 23, Appl
16	221	72.0	469	9	US-09-801-196-19	Sequence 19, Appl
17	221	72.0	469	9	US-09-853-386-100	Sequence 100, Appl
18	221	72.0	469	14	US-10-301-822-119	Sequence 119, Appl
19	221	72.0	469	14	US-10-021-660-76	Sequence 76, Appl
20	221	72.0	469	14	US-10-308-279-34	Sequence 34, Appl
21	221	72.0	469	14	US-10-131-985-23	Sequence 23, Appl
22	221	72.0	469	14	US-10-295-027-12	Sequence 12, Appl
23	221	72.0	469	14	US-10-295-027-14	Sequence 14, Appl
24	221	72.0	469	14	US-10-295-027-1167	Sequence 1167, Appl
25	221	72.0	469	14	US-10-295-027-1168	Sequence 1168, Appl
26	221	72.0	469	15	US-10-115-479-30	Sequence 30, Appl
27	221	72.0	469	15	US-10-115-479-40	Sequence 40, Appl
28	221	72.0	469	15	US-10-211-462-22	Sequence 22, Appl
29	221	72.0	469	15	US-10-188-832-6	Sequence 6, Appl
30	221	72.0	469	16	US-10-734-564-109	Sequence 109, Appl
31	221	72.0	470	15	US-10-447-315-1	Sequence 1, Appl
32	221	72.0	496	14	US-10-106-698-6283	Sequence 6283, Appl
33	214	69.7	54	14	US-10-219-329-9	Sequence 9, Appl
34	214	69.7	54	14	US-10-153-185-9	Sequence 9, Appl
35	214	69.7	54	14	US-10-219-561-9	Sequence 9, Appl
36	214	69.7	54	16	US-10-032-376A-9	Sequence 9, Appl
37	214	69.7	54	16	US-10-335-207-9	Sequence 9, Appl
38	198	64.5	173	15	US-10-115-479-48	Sequence 48, Appl
39	196	63.8	267	14	US-10-133-797-73	Sequence 73, Appl
40	196	63.8	477	9	US-09-391-104-21	Sequence 21, Appl
41	196	63.8	477	9	US-09-801-196-24	Sequence 24, Appl
42	196	63.8	477	14	US-10-171-311-137	Sequence 137, Appl
43	196	63.8	477	14	US-10-301-822-127	Sequence 127, Appl
44	196	63.8	477	14	US-10-131-985-27	Sequence 27, Appl
45	196	63.8	477	14	US-10-295-027-22	Sequence 22, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-219-329-10  
; Sequence 10, Application US/10219329  
; Publication No. US20030096757A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Weart, Fiona f.  
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds  
; FILE REFERENCE: 1443.035WO1  
; CURRENT APPLICATION NUMBER: US/10/219,329  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-329-10

Query Match 100.0%; Score 307; DB 14; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1e-32; Indels 0; Gaps 0;  
Matches 55; Conservative 0; Mismatches 0;  
CY 1 MORFFGLNVTGKPNBEETLDMKKPCRGVDSGGFMLTFCGNPKWERTNLTIRNY 55  
DB 1 MORFFGLNVTGKPNBEETLDMKKPCRGVDSGGFMLTFCGNPKWERTNLTIRNY 55

##### RESULT 2

US-10-153-185-10  
; Sequence 10, Application US/10153185  
; Publication No. US20030148959A1

Mon Nov 15 14:23:29 2004

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; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-185-10

Query Match      100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3
US-10-219-561-10
; Sequence 10, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Schail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-219-561-10

Query Match      100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55

US-10-032-376A-10
; Sequence 10, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21

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; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-376A-10

Query Match      100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MORFFGLNVTGKPNNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 5
US-10-335-207-10
; Sequence 10, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Schail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-335-207-10

Query Match      100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-391-104-24
; Sequence 24, Application US/09391104
; Publication No. US2002003187A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-24

Query Match      100.0%; Score 307; DB 9; Length 467;

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Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
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Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120  
RESULT 7  
US-09-801-196-20  
; Sequence 20, Application US/09801196  
; Patent No. US20020037827A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Kai  
; APPLICANT: Smith, Ryan  
; APPLICANT: Fajardo, Mark  
; APPLICANT: Moss, Patrick  
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)  
; FILE REFERENCE: 240083.509  
; CURRENT APPLICATION NUMBER: US/09/801,196  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-801-196-20  
Query Match 100.0%; Score 307; DB 9; Length 467;  
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Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120  
RESULT 8  
US-09-759-130B-176  
; Sequence 176, Application US/09759130B  
; Publication No. US2003002279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirt, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: MP100-5350NMIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364

; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 176  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-130B-176  
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Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55  
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120  
RESULT 9  
US-10-131-985-31  
; Sequence 31, Application US/10131985  
; Publication No. US2003019940A1  
; GENERAL INFORMATION:  
; APPLICANT: Dack, Kevin N  
; APPLICANT: Davies, Michael J  
; APPLICANT: Fish, Paul V  
; APPLICANT: Huggins, Jonathan P  
; APPLICANT: McIntosh, Fraser S  
; APPLICANT: Ocleston, Nicholas L  
; TITLE OF INVENTION: Composition  
; FILE REFERENCE: PCS 10391A  
; CURRENT APPLICATION NUMBER: US/10/131,985  
; CURRENT FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: US/09/726,295  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: GB 9930768.8  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-131-985-31  
Query Match 100.0%; Score 307; DB 14; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120  
RESULT 10  
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; Sequence 176, Application US/10741790  
; Publication No. US20040121396A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirt, Susan J

us-10-032-376a-10..rapb

Mon Nov 15 14:23:29 2004

APPLICANT: Mackay, Charles R  
 APPLICANT: Myers, Paul S  
 APPLICANT: Leiby, Kevin R  
 APPLICANT: Wrighton, Nicolas  
 APPLICANT: Goodearl, Andrew  
 APPLICANT: Holtzman, Douglas A  
 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
 TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
 TITLE OF INVENTION: USES  
 FILE REFERENCE: MP100-5350NM  
 CURRENT APPLICATION NUMBER: US/10/741,790  
 CURRENT FILING DATE: 2003-12-19  
 PRIOR APPLICATION NUMBER: US 09/479,249  
 PRIOR FILING DATE: 2000-01-07  
 PRIOR APPLICATION NUMBER: US 09/559,497  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: US 09/578,063  
 PRIOR FILING DATE: 2000-05-24  
 PRIOR APPLICATION NUMBER: US 09/333,159  
 PRIOR FILING DATE: 1999-06-14  
 PRIOR APPLICATION NUMBER: US 09/596,194  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 09/342,364  
 PRIOR FILING DATE: 1998-06-29  
 PRIOR APPLICATION NUMBER: US 09/608,452  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/393,996  
 PRIOR FILING DATE: 1998-09-10  
 PRIOR APPLICATION NUMBER: US 09/502,871  
 PRIOR FILING DATE: 2000-06-23  
 PRIOR APPLICATION NUMBER: US 09/420,707  
 PRIOR FILING DATE: 1999-10-19  
 NUMBER OF SEQ ID NOS: 460  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 176  
 LENGTH: 467  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MQRFFGLVNTGKNEETLDMKKPRCGVDSGGFMTLPGNPKWERTNLTIRNY 55  
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 RESULT 11  
 US-10-115-479-32  
 ; Sequence 32, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glendda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.

APPLICANT: Purtak, Katarzyna  
 APPLICANT: Patturajan, Meera  
 APPLICANT: Burgess, Catherine E.  
 APPLICANT: Malyanker, Uriel M.  
 APPLICANT: Shinkets, Richard A.  
 APPLICANT: Taupier, Raymond J.  
 APPLICANT: Edinger, Shlomit R.  
 APPLICANT: Mazur, Ann  
 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 FILE REFERENCE: 21402-322 B (Cura 622 PT)  
 CURRENT APPLICATION NUMBER: US/10/115,479  
 CURRENT FILING DATE: 2002-11-18  
 PRIOR APPLICATION NUMBER: 60/281,136  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/281,863  
 PRIOR FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/281,906  
 PRIOR FILING DATE: 2001-04-05  
 PRIOR APPLICATION NUMBER: 60/282,934  
 PRIOR FILING DATE: 2001-04-10  
 PRIOR APPLICATION NUMBER: 60/283,657  
 PRIOR FILING DATE: 2001-04-13  
 PRIOR APPLICATION NUMBER: 60/283,678  
 PRIOR FILING DATE: 2001-04-13  
 PRIOR APPLICATION NUMBER: 60/283,687  
 PRIOR FILING DATE: 2001-04-13  
 PRIOR APPLICATION NUMBER: 60/283,710  
 PRIOR FILING DATE: 2001-04-13  
 PRIOR APPLICATION NUMBER: 60/284,234  
 PRIOR FILING DATE: 2001-04-17  
 PRIOR APPLICATION NUMBER: 60/285,325  
 PRIOR FILING DATE: 2001-04-19  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 198  
 SEQ ID NO 32  
 LENGTH: 454  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-115-479-32

Query Match 72.0%; Score 221; DB 15; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.7e-20;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 Qy 1 MQRFFGLVNTGKNEETLDMKKPRCGVDSGGFMTLPGNPKWERTNLTIRNY 55  
 Db 50 MQRFFGLVNTGKNEETLDMKKPRCGVDSGGFMTLPGNPKWERTNLTIRNY 104  
 RESULT 12  
 US-10-115-479-34  
 ; Sequence 34, Application US/10115479  
 ; Publication No. US20040006205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gerlach, Valerie L.  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Zerhusen, Bryan D.  
 ; APPLICANT: Pena, Carol E.A.  
 ; APPLICANT: Shenoy, Suresh G.  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Smithson, Glendda  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Boldog, Ferenc L.;  
 ; APPLICANT: Voss, Edward  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: MacDougall, John A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malvanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 34  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-34

Query Match 72.0%; Score 221; DB 15; Length 454;  
Best Local Similarity 70.9%; Pred. No. 2.7e-20;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
OY 1 MQEFFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNKWEETNLTYIRNY 55  
DB 50 MQEFFGLKVTGKPDATLTKYMKQRCGVPDVAQFVLTEGNPRWEQTHLYRIENY 104

RESULT 13  
US-10-115-479-36  
Sequence 36, Application US/10115479  
Publication No. US2004006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malvanker, Uriel M.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO  
FILE REFERENCE: 21402-322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 36  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-36

Query Match 72.0%; Score 221; DB 15; Length 454;  
Best Local Similarity 70.9%; Pred. No. 2.7e-20;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
OY 1 MQEFFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNKWEETNLTYIRNY 55  
DB 50 MQEFFGLKVTGKPDATLTKYMKQRCGVPDVAQFVLTEGNPRWEQTHLYRIENY 104

RESULT 14  
US-10-115-479-38  
Sequence 38, Application US/10115479  
Publication No. US2004006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.

APPLICANT: Furtak, Katarzyna  
APPLICANT: Patturajan, Meera  
APPLICANT: Butgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402322 B (Cura 622 PT)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2003-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
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PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 38  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-38

Query Match 72.0%; Score 221; DB 15; Length 454;  
Best Local Similarity 70.9%; Pred. No. 2.7e-20;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFVMTPCNPKWERTNLTIRNY 55  
DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLTIRNY 104

RESULT 15  
US-09-391-104-23  
Sequence 23, Application US/093911104  
Publication No. US20020031817A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Falduto, Michael T.  
APPLICANT: Magnuson, Scott R.  
APPLICANT: Morgan, Douglas W.  
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.  
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
FILE REFERENCE: 6073.US.P1  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07  
PRIOR APPLICATION NUMBER: US 08/814,394  
PRIOR FILING DATE: 1997-03-11  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 469  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-391-104-23

Query Match 72.0%; Score 221; DB 9; Length 469;  
Best Local Similarity 70.9%; Pred. No. 2.8e-20;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFVMTPCNPKWERTNLTIRNY 55  
DB 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLTIRNY 121

Search completed: November 15, 2004, 14:22:34  
Job time : 142.436 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:35 ; Search time 12.3397 Seconds  
(without alignments)  
428.852 Million cell updates/sec

Title: US-10-032-376A-10  
Perfect score: 307  
Sequence: 1 MQRFFGLNVTGKPNNEETLDM.....LTPGNPKWERNLTLYRINY 55  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246014

Minimum DB seq length: 47  
Maximum DB seq length: 660

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collagenase
2	233	75.9	468	1 KCRBI	interstitial colla
3	231	75.2	469	1 KCPGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCB01	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 KCHUS3	stromelysin 3 (EC
10	193	62.9	477	1 KCHUS4	stromelysin 4 (EC
11	192	62.5	478	1 KCHUS5	stromelysin 5 (EC
12	190	61.9	476	1 KCHUS6	stromelysin 6 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KCHT1H	stromelysin 1 (EC
17	183	59.6	483	2 J55743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	matrilysin (EC 3.4
21	153	49.8	660	1 A28153	Gelatinase A (EC 3
22	138	45.0	462	2 A24201	macrophage elastas
23	134.5	43.8	582	2 I38028	matrix metalloprot
24	134.5	43.8	582	2 I34471	matrix metalloprot
25	129.5	42.2	582	2 I48673	matrix metalloprot
26	120	39.1	82	2 PWC052	pro-matrix metallo
27	111	36.2	521	1 T37252	probable matrix me
28	108	35.2	341	2 T51957	metalloproteinase
29	108	35.2	342	2 G84885	probable metallopr

30	104	33.9	364	2 E71433	probable metallopr
31	90	29.3	377	2 T00643	zinc metalloprotei
32	89.5	29.2	305	2 T08836	probable metallopr
33	89.5	29.2	378	2 E96724	hypothetical prote
34	88	28.7	488	2 S13423	stromelysin 3 (EC
35	85.5	27.9	616	2 JC7776	matrix metalloprot
36	83.5	27.2	477	1 I51645	stromelysin 3 (EC
37	82.5	26.9	579	2 T37248	probable matrix me
38	82.5	26.9	598	2 T32166	hypothetical prote
39	78	25.4	508	2 JC5082	matrix metalloprot
40	76.5	24.9	587	2 S12805	envelysin (EC 3.4.
41	75	24.4	491	2 JC6197	stromelysin 3 (EC
42	75	24.4	492	2 A44399	stromelysin 3 (EC
43	69.5	22.6	587	2 S41409	envelysin (EC 3.4.
44	61	19.9	592	2 F95277	probable dihydroxy
45	60.5	19.7	170	2 T17286	hypothetical prote

## ALIGNMENTS

RESULT 1  
KCHUN  
neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human  
N:Alternate names: matrix metalloproteinase 8  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text change 09-Jul-2004  
C/Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32527; S6  
R:Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev  
J. Biol. Chem. 265, 11421-11424, 1990  
A:Title: Human neutrophil collagenase. A distinct gene product with homology to other m  
A:Reference number: A37073; MUID:90307647; PMID:2164002  
A:Accession: A37073  
A:Molecule type: mRNA  
A:Residues: 1-467 <HAS>  
A:Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G18061  
R:Davajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.  
Blood 77, 2731-2738, 1991  
A:Title: Structure and expression of the cDNA encoding human neutrophil collagenase.  
A:Reference number: A61175; MUID:91255696; PMID:1646048  
A:Accession: A61175  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-31, 'I', '33-86, 'E', '88-467 <DEV>  
A:Accession: B61175  
A:Molecule type: protein  
A:Residues: 283-264, 'X', '266-270, 'X', '272-273, 'X', '275, 'X', '277 <D22>  
R:Malya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.;  
Biochemistry 29, 10628-10634, 1990  
A:Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison wit  
A:Reference number: A36230; MUID:91104978; PMID:2176876  
A:Accession: A36230  
A:Molecule type: protein  
A:Residues: 'X', '86-87, 'X', '89-90, 'X', '92-97, 'X', '99-111, 'X', '113-120 <MAL>  
R:Knauper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
Eur. J. Biochem. 189, 295-300, 1990  
A:Title: Characterization and activation of procollagenase from human polymorphonuclear  
A:Reference number: S09680; MUID:90249372; PMID:2159879  
A:Accession: S09680  
A:Molecule type: protein  
A:Residues: 21-31, 'I', '33-39, 'I', '41-47, 'V', '49-53, 'I', '55-72, 'G', '74-86, 'E', '88-111, 'X', '113-  
A>Note: 67-Lys was also found  
R:Knauper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
Biol. Chem. Hoppe-Seyler 371, 733, 1990  
A:Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase  
A:Reference number: S11026; MUID:91000455; PMID:2169766  
A>Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990  
A:Accession: S11026  
A:Molecule type: protein  
A:Residues: 21-31, 'I', '33-53, 'I', '55-72, 'G', '74-111, 'X', '113-140, '183-203, 'X', '205-209, '248-26  
A>Note: 87-Glu was also found  
R:Blaser, J.; Knauper, V.; Osthues, A.; Reinke, H.; Tschesche, H.  
Eur. J. Biochem. 202, 1223-1230, 1991

RESULT 2  
KCRBI  
A:Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.  
A:Reference number: S19576; MUID:92111500; PMID:1662606  
A:Accession: S19576  
A:Molecule type: Protein  
A:Residues: 69-103 <Bu2>  
R:Blaser, J.; Triebel, S.; Reinke, H.; Tschesche, H.  
FEBS Lett. 313, 59-61, 1992  
A:Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.  
A:Reference number: S27225; MUID:93050220; PMID:1330697  
A:Accession: S27225  
A:Molecule type: Protein  
A:Residues: 68-103 <BuA>  
R:Knaeuper, V.; Osthus, A.; Declerck, Y.A.; Langley, K.E.; Blaaser, J.; Tschesche, H.  
Biochem. J. 291, 847-854, 1993  
A:Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.  
A:Reference number: S32527; MUID:93256897; PMID:8489511  
A:Accession: S32527  
A:Molecule type: Protein  
A:Residues: 100-112:263-276 <KN3>  
R:Knaeuper, V.; Murphy, G.; Tschesche, H.  
Eur. J. Biochem. 235, 187-191, 1996  
A:Title: Activation of human neutrophil procollagenase by stromelysin 2.  
A:Reference number: S62608; MUID:96202934; PMID:8631328  
A:Accession: S62608  
A:Molecule type: Protein  
A:Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>  
R:Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.  
Submitted to the Brookhaven Protein Data Bank, January 1994  
A:Reference number: A67078; PDB:1MNC  
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1  
R:Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahi, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, N.A.  
Struct. Biol. 1, 119-123, 1994  
A:Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.  
A:Reference number: A58274; MUID:95384762; PMID:7656015  
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1  
C:Comment: This protein is more highly glycosylated than interstitial collagenase and is  
C:Genetics:  
A:Gene: GDB:MMP8; CLG1  
A:Cross-references: GDB:128173; OMIM:120355  
A:Map position: 11q22.2-11q22.3  
C:Function:  
A:Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous  
A:Note: cleaves type I collagen most rapidly  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase  
C:Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-467/Product: procollagenase #status predicted <PRO>  
F:21-100/Domain: activation peptide #status experimental <ACT>  
F:59-262/Domain: matrix metalloproteinase homology <MMP>  
F:89-96/Region: autoinhibitory  
F:101-467/Product: neutrophil collagenase #status predicted <MAT>  
F:273-464/Domain: hemopexin repeat homology <PXN>  
F:54,73,112,119,204,246/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:73-74/Cleavage site: Asn-Val (autolytic) #status experimental  
F:84-85/Cleavage site: Asp-Met (autolytic) #status experimental  
F:91-217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:99-100/Cleavage site: Phe-Met (autolytic) #status experimental  
F:167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime  
F:174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e  
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental  
F:218/Active site: Glu #status predicted  
F:262-263/Cleavage site: Gly-Leu (autolytic) #status experimental  
F:279-464/Disulfide bonds: #status predicted

Query Match 100.0%; Score 307; DB 1; Length 467;  
Best Local Similarity 100.0%; Pred. No. 6,7e-31;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKPNBETLDMKKPCRGVDPDGGFMTLPGNPKWERTNLTIRNY 55  
|||||  
Db 66 MORFFGLNVTGKPNBETLDMKKPCRGVDPDGGFMTLPGNPKWERTNLTIRNY 120  
|||||

RESULT 2  
KCRBI  
A:Title: Interstitial collagenase (EC 3.4.24.7) precursor - rabbit  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A27500; E27500; I46694  
R:Finzi, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.  
Biochemistry 26, 6156-6165, 1987  
A:Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote  
A:Reference number: A27500; MUID:88077876; PMID:2825772  
A:Accession: A27500  
A:Molecule type: mRNA  
A:Residues: 1-468 <FIN>  
A:Cross-references: UNIPROT:P13943; GB:M19240  
A:Accession: B27500  
A:Molecule type: DNA  
A:Residues: 1-391:399-468 <F12>  
A:Cross-references: GB:M17820  
A:Note: the location of the intron between exons 7 and 8 is approximate  
R:Finzi, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho  
Coll. Relat. Res. 6, 239-248, 1986  
A:Title: Homology between exon-containing portions of rabbit genomic clones for synovial  
A:Reference number: I46694; MUID:87029174; PMID:3021384  
A:Accession: I46694  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 449-468 <F13>  
A:Cross-references: GB:M25663; NID:G531211; PIDN:AAA31203.1; PID:9531212  
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th  
C:Comment: Procollagenase can be activated without removal of the activation peptide. St  
tion peptide by other proteinases.  
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C:Genetics:  
A:Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1  
C:Function:  
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-468/Product: procollagenase #status predicted <PRO>  
F:19-98/Domain: activation peptide #status predicted <ACT>  
F:59-260/Domain: matrix metalloproteinase homology <MMP>  
F:89-96/Region: autoinhibitory  
F:91-465/Domain: hemopexin repeat homology <PXN>  
F:91-217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F:119,142/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted  
F:218/Active site: Glu #status predicted  
F:279-465/Disulfide bonds: #status predicted

Query Match 75.9%; Score 233; DB 1; Length 468;  
Best Local Similarity 74.5%; Pred. No. 1.6e-21;  
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKPNBETLDMKKPCRGVDPDGGFMTLPGNPKWERTNLTIRNY 55  
|||||  
Db 66 MORFFGLNVTGKPNBETLDMKKPCRGVDPDGGFMTLPGNPKWERTNLTIRNY 120  
|||||

RESULT 3  
KCPGI  
A:Title: Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: S15986; S1597  
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.  
Matrix 11, 161-167, 1991  
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of  
A:Reference number: S15986; MUID:91333421; PMID:1651440  
A:Accession: S15986



A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-469 <RES>  
A:Cross-references: UNIPROT:P21692  
A>Note: part of the sequence, including the amino end of the proenzyme, was confirmed by R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.  
Nucleic Acids Res. 18, 6703, 1990  
A>Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.  
A:Reference number: S13597; MUID:91067477; PMID:2174547  
A:Accession: S13597  
A:Molecule type: mRNA  
A:Residues: 25-469 <CLA>  
A:Cross-references: EMBL:X54724; NID:G2016; PIDN:CAA38526.1; PID:9930269  
R;Li, J.; Brick, P.; Blow, D.M.  
submitted to the Brookhaven Protein Data Bank, April 1995  
A:Reference number: A65568; PDB:1PBL  
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466  
C;Comment: Procollagenase can be activated without removal of the activation peptide. St  
tion peptide by other proteinases.  
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C;Function:  
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
A>Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F1-13/Domain: signal sequence #status predicted <SIG>  
F20-469/Product: procollagenase #status predicted <PRO>  
F20-59/Domain: activation peptide #status experimental <ACT>  
F60-261/Domain: matrix metalloproteinase homology <MMP>  
F100-469/Product: interstitial collagenase #status predicted <MAT>  
F272-466/Domain: hemopexin repeat homology <PXN>  
F92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
F218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
F219/Active site: Glu #status predicted  
F278-466/Disulfide bonds: #status experimental

Query Match 75.2%; Score 231; DB 1; Length 469;  
Best Local Similarity 72.7%; Pred. No. 2.8e-21;  
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORFGLNVTGKPNETLDMKKPCGVPDSCGFMLTQGNPKWERTNLTIRNY 55  
Db 67 MQQFGLKVTGKPDATLNMVQPCGVPDVAEFVITFGNPRWENTHTYRIEN 121

RESULT 4  
KCHUI  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
C:Species: Homo sapiens (man)  
C:Date: 13-Aug-1986 #sequence, revision 30-Sep-1992 #text change 09-Jul-2004  
C:Accession: A3708; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S53  
R;Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St  
Cancer Res. 50, 5431-5437, 1990  
A>Title: Cloning and characterization of human tumor cell interstitial collagenase.  
A:Reference number: A37308; MUID:90352887; PMID:2167156  
A:Accession: A37308  
A:Molecule type: mRNA  
A:Residues: 1-469 <TEM>  
A:Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126  
R;Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.  
J. Clin. Invest. 79, 542-546, 1987  
A>Title: Molecular cloning of human synovial cell collagenase and selection of a single  
A:Reference number: S22766; MUID:87109799; PMID:3027129  
A:Accession: S22766  
A:Molecule type: DNA  
A:Residues: 1-63,65-70 <BRI>  
A:Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667  
R;Angel, P.; Baumann, I.; Stein, B.; Dalius, H.; Rahmsdorf, H.J.; Herrlich, P.  
Mol. Cell. Biol. 7, 2256-2266, 1987  
A>Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene  
A:Reference number: I57620; MUID:87257941; PMID:3037355

A:Accession: I57620  
A>Status: preliminary; translated from GB/EMBL/DBDJB  
A:Molecule type: DNA  
A:Residues: 1-35 <RES>  
A:Cross-references: GB:M16567; NID:G180668; PIDN:AAA52033.1; PID:G180669  
R;Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.  
J. Biol. Chem. 261, 6600-6605, 1986  
A>Title: Human fibroblast collagenase. Complete primary structure and homology to an on  
A:Reference number: A00996; MUID:86196089; PMID:3009463  
A:Accession: A00996  
A:Molecule type: mRNA  
A:Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>  
A:Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665  
A>Note: part of this sequence was confirmed by protein sequencing of the proenzyme  
R;Witham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris  
Biochem. J. 240, 913-916, 1986  
A>Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis  
A:Reference number: A90336; MUID:87156645; PMID:3030290  
A:Accession: D29157  
A:Molecule type: mRNA  
A:Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>  
A:Cross-references: EMBL:X55231; NID:G38266; PIDN:CAA28858.1; PID:G38267  
A>Note: parts of this sequence, including the amino end of the proenzyme and of the mat  
R;Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Shown, A.S.; Birkedal-Hansen, H.  
Biochemistry 27, 6751-6758, 1988  
A>Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzyme  
end of the activated enzyme.  
A:Reference number: A44518; MUID:89062403; PMID:2461732  
A:Accession: A44518  
A:Molecule type: protein  
A:Residues: 270-305 <BIR>  
R;Clark, I.M.; Cawston, T.E.  
Biochem. J. 263, 201-206, 1989  
A>Title: Fragments of human fibroblast collagenase. Purification and characterization.  
A:Reference number: S06132; MUID:90104231; PMID:2557822  
A:Accession: S06132  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 100-102, 'P', 104-107, 'XX', 110-112, 270-277, 'X', 279-280, 'X', 282-287 <CLA>  
R;Rak, M.W.; Walakovits, L.A.; Shah, T.K.; Vammildesworth, J.; Cameton, P.M.; Lin, T.  
Connect. Tissue Res. 25, 49-65, 1990  
A>Title: Production and purification of prostromelysin and procollagenase from IL-1 bet  
A:Reference number: A60964; MUID:91059606; PMID:2173990  
A:Accession: B60964  
A:Molecule type: protein  
A:Residues: 24-35; 100-108; 270-272, 'X', 274, 'X', 276 <LAR>  
R;Suzuki, K.; Nagase, H.; Ito, A.; Englund, J.J.; Salvesen, G.  
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990  
A>Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rhe  
A:Reference number: S10595; MUID:90380300; PMID:2169257  
A:Accession: S10595  
A:Molecule type: protein  
A:Residues: 20-102 <SUZ>  
R;Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.  
Biochem. J. 305, 301-306, 1995  
A>Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collage  
A:Reference number: S53438; MUID:95126921; PMID:7826345  
A:Accession: S53438  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 20-108 <SU2>  
R;Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.  
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990  
A>Title: Multiple modes of activation of latent human fibroblast collagenase: evidence  
A:Reference number: A44517; MUID:90115877; PMID:2153297  
A:Contents: annotation; disulfide bond; activation mechanism  
R;Salowe, S.P.; Marcy, A.I.; Cuca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Herme  
Biochemistry 31, 4535-4540, 1992  
A>Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry o  
A:Reference number: A43031; MUID:92256384; PMID:1581308  
A:Contents: annotation; zinc ligand in proenzyme  
A>Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the cata  
C;Comment: Procollagenase can be activated without removal of the activation peptide. S

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted

A;Accession: A28399  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation

F;219/Active site: Glu #status predicted  
F;290-477/Disulfide bonds: #status predicted

Query Match 63.8%; Score 196; DB 1; Length 477;  
Best Local Similarity 63.6%; Pred. No. 7.8e-17;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFGLVNTGKNEETLDMKKPRCGVPDSGGFMLTPGNPKWERTNLTYYRNY 55  
Db 67 MQRFGLGVTKLSDTLEWVRKPRCGVPDVGHFRTFPGIPKWRKTLTYRINY 121

RESULT 8  
KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human  
N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A28816; A47496  
R;Muller, D.; Quantin, B.; Genel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, A.; Biochem. J. 253, 187-192, 1988  
A;Title: The collagenase gene family in humans consists of at least four members.  
A;Reference number: A90339; MUID:88339885; PMID:2844164  
A;Accession: A28916  
A;Molecule type: mRNA  
A;Residues: 1-476 <MUL>  
A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:g36628; PIDN:CAA30679.1; PID:g3662  
A;Note: mRNA for this protein was detected in several human tumors  
R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Borden, M.K.; Engler, J.A.; Birkedal  
J. Biol. Chem. 268, 17341-17347, 1993  
A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene  
A;Reference number: A47496; MUID:9332520; PMID:8349617  
A;Accession: A47496  
A;Molecule type: protein  
A;Residues: 17-33 <WIN>  
C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
C;Genetics:  
A;Gene: GDB:MMP10; STMY2  
A;Cross-references: GDB:120392; OMIM:185260  
A;Map position: 11q22.3-11q23  
A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-476/Product: prostromelysin 2 #status experimental <PRO>  
F;17-98/Domain: activation peptide #status predicted <ACT>  
F;59-263/Domain: matrix metalloproteinase homology <MMP>  
F;89-96/Region: autoinhibitory  
F;95-476/Product: stromelysin 2 #status predicted <MAT>  
F;203-476/Domain: hemopexin repeat homology <PXN>  
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;119/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted  
F;218/Active site: Glu #status predicted  
F;289-476/Disulfide bonds: #status predicted

Query Match 63.5%; Score 195; DB 1; Length 476;  
Best Local Similarity 63.6%; Pred. No. 1e-16;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFGLVNTGKNEETLDMKKPRCGVPDSGGFMLTPGNPKWERTNLTYYRNY 55  
Db 66 MQRFGLGVTKLSDTLEWVRKPRCGVPDVGHFRTFPGIPKWRKTLTYRINY 120

RESULT 9  
JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse  
N;Alternate names: matrix metalloproteinase 10  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Oct-1998 #sequence\_revision 16-Oct-1998 #text\_change 09-Jul-2004  
C;Accession: JC6505  
R;Madlener, M.; Werner, S.  
Gene 202, 75-81, 1997



**RESULT 12**

KRIS2

stromelysin 2 (EC 3.4.24.22) precursor - rat  
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: B26403; A41775; S26498  
R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.  
Nucleic Acids Res. 15, 1139-1151, 1987  
A>Title: Sequences coding for part of oncogene-induced transin are highly conserved in a  
A:Reference number: A26403; MUID:87146421; PMID:3547333  
A:Accession: B26403  
A:Molecule type: mRNA  
A:Residues: 1-476 <BRE>  
A:CROSS-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PID:NCAA28739.1; PID:Q57389  
A>Note: Intron positions were determined by comparison of the cDNA sequence to genomic s  
A:Note: mRNA for this protein was expressed in several transformed rat embryo fibroblast  
J.Chan, J.C.; Scallan, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Ea  
R. Biol. Chem. 267, 1099-1103, 1992  
A>Title: Molecular cloning and characterization of v-mos-activated transformation-associ  
A:Reference number: A41775; MUID:92112748; PMID:1370458  
A:Accession: A41775  
A:Molecule type: mRNA  
A:Residues: 1-476 <CHA>  
A:CROSS-references: GS:M65253; NID:G207150; PID:AAA42202.1; PID:G207151  
A:Note: Sequence extracted from NCBI backbone (NCBIP:76184)  
R.de Vouge, M.W.; Mukherjee, B.B.  
Oncogene 7, 102-119, 1993  
A>Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra  
A:Reference number: B26496; MUID:92158347; PMID:1741158  
A:Accession: B26498  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 31-103, 'L', 241-242, 'TQWEERPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>  
A:CROSS-references: EMBL:X64020  
C:Genetics:  
F:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
P:1-17/Domain: signal sequence #status predicted <SIG>  
P:18-476/Product: prostromelysin 2 #status predicted <PRO>  
P:18-99/Domain: activation peptide #status predicted <ACT>  
P:180-264/Domain: matrix metalloproteinase homology <MMP>  
P:190-97/Region: autoinhibitory  
F:100-476/Product: stromelysin 2 #status predicted <MAT>  
F:283-476/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #stratus  
F:120/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F:219/Active site: Glu #status predicted  
F:289-476/disulfide bonds: #status predicted

Query Match 61.9%; Score 190; DB 1; Length 476;  
Best Local Similarity 58.2%; Pred No. 4.5e-16;  
Matches 32; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Oy 1 MQRFGLNVTKPNETLDMMKPRCGVPDPSGGFMLTGPKNPKWERTNLTYIRNY 55  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 67 MQKPLGLEMTGKLDSNTVENMKHPRCGVDPVGGSFTFGSPKKXKHISRIVNY 121  
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

**RESULT 13**

A23695

interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)  
N:Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
C:Accession: A23685  
R:Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge  
J. Biol. Chem. 265, 22342-22347, 1990  
A>Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone

A:Gene: GDB:MMP13; CLG3  
A:Cross-references: GDB:373966; OMIM:600108  
A:Map position: 11q22.2-11q22.3  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease  
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F:64-267/Domain: matrix metalloproteinase homology <MMP>  
F:278-471/Domain: hemopexin repeat homology <PXN>  
F:96,222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted  
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;  
Best Local Similarity 63.6%; Pred. No. 7.9e-16;  
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
Db 71 MOSFFELEVTGKLDNTLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 125

Search completed: November 15, 2004, 14:07:19  
Job time : 12.3397 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:01:34 ; Search time 50.7692 Seconds  
(without alignments)  
623.323 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLVTKPNEETLDM.....LTPGNKWTNTLYIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1605865

Minimum DB seq length: 47

Maximum DB seq length: 660

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 MM08 HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01 RABIT	F13943 coryctolagus
3	231	75.2	469	1 MM01 PIG	P21692 sus scrofa
4	223	72.6	466	1 MM08 RAT	O88766 rattus norv
5	222	72.3	469	1 MM01 HORSE	Q9X525 equus cabal
6	221	72.0	469	1 MM01 HUMAN	P03956 homo sapien
7	221	72.0	469	2 AAP35520	AAP35520 homo sapi
8	218	71.0	469	1 MM01 BOVIN	P28053 bos taurus
9	201.5	65.6	384	1 MM01 RANCA	Q11133 rana catesb
10	198	64.5	465	2 Q8C209	Q8C209 mus musculu
11	198	64.5	465	2 Q8C230	Q8C230 mus musculu
12	198	64.5	465	2 AAH42742	AAH42742 mus muscu
13	198	64.5	465	2 BAC40805	BAC40805 mus muscu
14	198	64.5	478	2 O6Y405	O6Y405 canis fami
15	198	64.5	478	2 AAP63580	AAP63580 canis fam
16	196	63.8	469	1 MM13 XENLA	Q10835 xenopus lae
17	196	63.8	472	2 Q93342	Q93342 gallus gall
18	196	63.8	472	2 Q10833	Q10833 xenopus lae
19	196	63.8	477	1 MM03 HUMAN	P08254 homo sapien
20	196	63.8	477	2 AAH69676	AAH69676 homo sapi
21	196	63.8	477	2 AAH69716	AAH69716 homo sapi
22	195	63.5	476	1 MM10 HUMAN	P09238 homo sapien
23	195	63.5	476	2 AAP36110	AAP36110 homo sapi
24	194	63.2	145	2 Q9N283	Q9N283 bos taurus
25	194	63.2	452	2 Q9T182	Q9T182 canis fami
26	193	62.9	476	1 MM10 MOUSE	O51123 mus musculu
27	193	62.9	477	1 MM03 MOUSE	P28862 mus musculu
28	193	62.9	479	2 Q922W6	Q922W6 mus musculu
29	192	62.5	478	1 MM03 RABIT	P28863 coryctolagus
30	190	61.9	465	1 MM08 MOUSE	O70138 mus musculu
31	190	61.9	476	1 MM10 RAT	P07152 rattus norv

32 189 61.6 466 1 MM13 RAT  
33 189 61.6 472 1 MM13 MOUSE  
34 188 61.2 383 2 Q7Z5M0  
35 188 61.2 393 2 O8MI18  
36 188 61.2 471 1 MM13 HUMAN  
37 188 61.2 471 2 Q6NM66  
38 188 61.2 471 2 AAH67522  
39 188 61.2 471 2 AAH67523  
40 188 61.2 475 1 MM03 RAT  
41 188 61.2 489 2 Q7Z5M1  
42 187 60.9 472 1 MM13 HORSE  
43 185 60.3 139 2 O3QM68  
44 185 60.3 471 1 MM13 BOVIN  
45 184 59.9 259 2 Q6DF35

#### ALIGNMENTS

##### RESULT 1.

MM08\_HUMAN  
ID MM08\_HUMAN STANDARD; PRT; 467 AA.  
AC P22894;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).  
GN Name=MMP8; Synonyms=CLG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90307647; PubMed=2164002;  
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P., Spinella D.G., Stevens R.M., Mainardi C.L.;  
RT "Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.";  
RL J. Biol. Chem. 265:11421-11424(1990).  
RN [2]  
RP SEQUENCE OF 21-140.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90249372; PubMed=2159879;  
RA Kraeuper V., Kraeuper S., Reinke H., Tschesche H.;  
RT "Characterization and activation of procollagenase from human polymorphonuclear leucocytes. N-terminal sequence determination of the proenzyme and various proteolytically activated forms.";  
RL Eur. J. Biochem. 189:295-300(1990).  
RN [3]  
RP SEQUENCE OF 21-103.  
RC TISSUE=Neutrophils;  
RX MEDLINE=92111500; PubMed=1662606;  
RA Blaesser J., Kneuper V., Osthus A., Reinke H., Tschesche H.;  
RT "Mercurial activation of human polymorphonuclear leucocyte procollagenase.";  
RL Eur. J. Biochem. 202:1223-1230(1991).  
RN [4]  
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91104978; PubMed=2176876;  
RA Malliyil S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M., Birkedal-Hansen H., van Wart H.E.;  
RT "Characterization of 58-kilodalton human neutrophil collagenase: comparison with human fibroblast collagenase.";  
RL Biochemistry 29:10628-10634(1990).  
RN [5]  
RP PARTIAL SEQUENCE.  
RX MEDLINE=90380298; PubMed=2169256;  
RA Kneuper V., Kraeuper S., Reinke H., Tschesche H.;  
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";

P23097 rattus norv  
P33435 mus musculu  
Q725M0 homo sapien  
O8MI18 felis silve  
P45452 homo sapien  
Q6NM66 homo sapien  
AAH67522 homo sapi  
AAH67523 homo sapi  
P03957 rattus norv  
O7Z5M1 homo sapien  
O18927 equus cabal  
Q3QM68 sus scrofa  
O76566 bos taurus  
Q6DF35 xenopus tro





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FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.

Query Match
Best Local Similarity 100.0%; Score 307; DB 1; Length 467;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 2
MM01_RABIT
ID MM01_RABIT STANDARD; PRT; 468 AA.
AC PI3943;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=8807876; PubMed=2825772;
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
RT "A gene for rabbit synovial cell collagenase: member of a family of
RT metalloproteinases that degrade the connective tissue matrix.";
RL Biochemistry 26:6156-6165(1987).
RN [2]_
RP SEQUENCE OF 449-468 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=87029174; PubMed=3021384;
RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
RA Brinckerhoff C.E.;
RT "Homology between exon-containing portions of rabbit genomic clones
RT for synovial cell collagenase and human foreskin and synovial cell
RT mRNAs.";
RL Coll. Relat. Res. 6:239-248(1986).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where Pi' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M17823; AAB88016.1; -
CC EMBL; M17820; AAB88016.1; JOINED.
CC EMBL; M17821; AAB88016.1; JOINED.
CC EMBL; M17822; AAB88016.1; JOINED.
CC EMBL; M19240; AAB88016.1; JOINED.
CC EMBL; M25663; AAA31203.1; -

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DR PIR; A27500; KCRB1.
DR HSSP; P03956; 1CGL.
DR MEROPS; M10.001; -.
DR InterPro; IP000585; Hemopexin.
DR InterPro; IP0005026; Peptidase_M.
DR InterPro; IP0001818; Pept_M10A_M12B.
DR InterPro; IP0006025; Pept_M_Zn_BS.
DR InterPro; IP0009070; PGSD-like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 18 Activation peptide.
FT PROPEP 19 98 Interstitial collagenase.
FT CHAIN 99 468 Hemopexin-like.
FT DOMAIN 274 468 Cysteine switch (Potential).
FT SITE 91 91 Calcium 1 (By similarity).
FT METAL 123 123 Calcium 2 (By similarity).
FT METAL 157 157 Zinc 1 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Calcium 3 (By similarity).
FT METAL 174 174 Calcium 3 (via carbonyl oxygen)
FT METAL 175 175 similarity).
FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
FT METAL 179 179 similarity).
FT METAL 182 182 Calcium 3 (via carbonyl oxygen) (By
FT METAL 189 189 similarity).
FT METAL 191 191 Zinc 1 (By similarity).
FT METAL 193 193 Calcium 2 (via carbonyl oxygen) (By
FT METAL 195 195 similarity).
FT METAL 197 197 Calcium 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 200 200 Calcium 1 (By similarity).
FT METAL 217 217 Calcium 3 (By similarity).
FT ACT_SITE 218 217 Zinc 2 (catalytic) (By similarity).
FT METAL 221 221 Zinc 2 (catalytic) (By similarity).
FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
FT METAL 284 284 Calcium 4 (via carbonyl oxygen) (By
FT METAL 328 328 similarity).
FT METAL 377 377 Calcium 4 (via carbonyl oxygen) (By
FT METAL 426 426 similarity).
FT CARBOHYD 119 119 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 277 465 similarity).
FT SEQUENCE 468 AA; 53739 MW; DA9053891952B8C CRC64;
Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 4.3e-20;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MOEFFGLKVTGKPEADETLKMOKQPCRGVDSVAQFVLTPGNPWEQTHLTIRNY 120

RESULT 3
MM01_PIG

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ID AC MM01\_PIG STANDARD; PRT; 469 AA.  
DI P21692;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
DE metalloproteinase-1) (MMP-1).  
GN Name=MMP1;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=91333421; PubMed=1651440;  
RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.,  
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and  
RT modulation of expression of RNA in vitro by various cytokines.";  
RL Matrix 11:161-167(1991).  
RN [2]  
RP SEQUENCE OF 25-469 FROM N.A.  
RC TISSUE=Synovial cell;  
RX MEDLINE=91067477; PubMed=2174547;  
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;  
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,  
RT obtained by PCR.";  
RL Nucleic Acids Res. 18:6703-6703(1990).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.  
RX MEDLINE=9617303; PubMed=8590015;  
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,  
RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;  
RT "Structure of full-length porcine synovial collagenase reveals a C-  
RT terminal domain containing a calcium-linked, four-bladed beta-  
RT propeller.";  
RL Structure 3:541-549(1995).  
RN [4]  
RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.  
RX MEDLINE=95142615; PubMed=7940605;  
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,  
RA O'Hare M.C.;  
RT "Recombinant porcine collagenase: purification and autolysis.";  
RL Arch. Biochem. Biophys. 316:123-127(1995).  
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
CC the helical domain. Also cleaves collagens of types VII and X.  
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
CC collagen. Cleavage of the triple helix of collagen at about three-  
CC quarters of the length of the molecule from the N-terminus, at  
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
CC substrates and alpha-macroglobulins at bonds where Pi' is a  
CC hydrophobic residue.  
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -!- ENZYME REGULATION: Can be activated without removal of the  
CC activation peptide.  
CC -!- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment  
CC having reduced collagenolytic activity.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X54724; CAA38526.1; -.  
DR PIR; S15986; KCFGI.  
DR PDB; 1FBL; X-ray; @=100-469.  
DR MEROPS; M10.001; -.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase\_M.

DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR009070; PGBD\_like.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; SM00138; MATRIXIN.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZmMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW 3D-structure; Autocatalytic cleavage; Calcium-binding;  
KW Collagen degradation; Direct protein sequencing; Extracellular matrix;  
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
KW Zymogen.  
FT SIGNAL 1 19  
FT PROPEP 20 99 Activation peptide.  
FT CHAIN 100 469 Interstitial collagenase.  
FT CHAIN 100 258 18 kDa interstitial collagenase.  
FT DOMAIN 275 489 Hemopexin-like. (Potential).  
FT SITE 92 92 Cysteine switch (autolytic).  
FT SITE 258 259 Cleavage (autolytic).  
FT METAL 124 124 Calcium 1.  
FT METAL 158 158 Calcium 2.  
FT METAL 168 168 Zinc 1.  
FT METAL 170 170 Zinc 1.  
FT METAL 175 175 Calcium 3.  
FT METAL 176 176 Calcium 3 (via carbonyl oxygen).  
FT METAL 178 178 Calcium 3 (via carbonyl oxygen).  
FT METAL 180 180 Calcium 3 (via carbonyl oxygen).  
FT METAL 183 183 Zinc 1.  
FT METAL 190 190 Calcium 2 (via carbonyl oxygen).  
FT METAL 192 192 Calcium 2 (via carbonyl oxygen).  
FT METAL 194 194 Calcium 2.  
FT METAL 196 196 Zinc 1.  
FT METAL 198 198 Calcium 3.  
FT METAL 199 199 Calcium 1.  
FT METAL 201 201 Calcium 3.  
FT METAL 218 218 Zinc 2 (catalytic).  
FT ACT\_SITE 219 219 Zinc 2 (catalytic).  
FT METAL 222 222 Zinc 2 (catalytic).  
FT METAL 228 228 Calcium 4 (via carbonyl oxygen).  
FT METAL 285 285 Calcium 4 (via carbonyl oxygen).  
FT METAL 329 329 Calcium 4 (via carbonyl oxygen).  
FT METAL 378 378 Calcium 4 (via carbonyl oxygen).  
FT METAL 427 427 Calcium 4 (via carbonyl oxygen).  
FT DISULFID 278 466 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 120 120  
FT STRAND 101 102  
FT TURN 104 105  
FT STRAND 113 118  
FT TURN 123 124  
FT STRAND 127 142  
FT HELIX 143 144  
FT TURN 148 152  
FT STRAND 159 164  
FT STRAND 182 184  
FT TURN 190 193  
FT STRAND 195 198  
FT TURN 199 200  
FT STRAND 204 204  
FT STRAND 211 211  
FT HELIX 212 223  
FT TURN 224 225  
FT STRAND 226 227  
FT TURN 232 233  
FT TURN 235 236  
FT HELIX 250 260  
FT TURN 277 278  
FT TURN 280 281  
FT STRAND 286 290  
FT TURN 291 292

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FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT HELIX 364 368
FT TURN 372 373
FT STRAND 379 383
FT TURN 384 387
FT STRAND 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 7.6e-20;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNETLDMKKKPGVDPDSGFMLTIPGNKWEINLTITIRNY 55
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 MQQFFGLKVTGTPDAETLNWKPQRCGVPDVAEFLVTFGNFRWENTHLYTIENY 121

Db

RESULT 4
MM08 RAT STANDARD; PRT; 466 AA.
AC O88766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowe D., Wells G., Burel S., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By

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similarity).
-!- ENZYME REGULATION: Cannot be activated without removal of the activation peptide (By similarity).
-!- SUBCELLULAR LOCATION: Stored in intracellular granules.
-!- SIMILARITY: Belongs to peptidase family M10A.
-!- SIMILARITY: Contains 1 hemopexin-like domain.
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EMBL; AJ007288; CAA07432.1; --
HSP; P22894; IZS.
MEROPS; M10.002; --
InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Pept_M10A_M12B.
InterPro; IPR006025; Pept_M_Zn_BS.
InterPro; IPR009070; PGBD_like.
Pfam; PF00045; Hemopexin_4.
Pfam; PF00413; Peptidase_M10; 1.
Pfam; PF03933; Peptidase_M10_N; 1.
PRINTS; PR00138; MATRIXIN.
PROSITE; PS00546; CYSTEINE_SWITCH; 1.
PROSITE; PS00024; HEMOPEXIN; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Calcium-binding; Collagen degradation; Extracellular matrix;
Calcium-binding; Hydroxylase; Metal-binding; Metalloprotease; Signal; Zinc;
Glycoprotein; Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 By similarity.
FT METAL 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 379 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 426 Calcium 3 (via carbonyl oxygen) (By similarity).
FT DISULFID 280 Probable.
FT CARBOHYD 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;

Query Match 72.8%; Score 223; DB 1; Length 466;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;

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Matches 39; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDGGFMTGPNKQWERTNLTIRNY 55  
 DB 67 MQRFFGLNVTGKPNBETLDMKKPCGVPDGGFMTGPNKQWERTNLTIRNY 121

RESULT 5

MM01\_HUMAN STANDARD; PRT; 469 AA.

AC Q9X3Z5;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).  
 GN Name=MMP1;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Richardson D.W.;  
 RT "Cloning and expression of equine matrix metalloproteinase 1 (interstitial collagenase).";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).  
 CC -!- ENZYME REGULATION: Can be activated without removal of the activation peptide.  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.

-----

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-----

DR EMBL; AF148882; AAD38030.1; --  
 DR HSSP; P03956; 1AYK.  
 DR MEROPS; M10.001; --  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGSD-like.  
 DR Pfam; PF00445; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRXIN.  
 DR SMART; SM00120; HK; 4.  
 DR SMART; SM00235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Calcium-binding; Collagen degradation; Extracellular matrix;  
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
 KW Zymogen.  
 FT SIGNAL 1 18 By similarity.  
 FT PROPEP 19 99 Activation peptide.  
 FT CHAIN 100 469 Interstitial collagenase.

FT DOMAIN 275 469 Hemopexin-like.  
 FT SITE 92 Cysteine switch (Potential).  
 FT METAL 124 Calcium 1 (By similarity).  
 FT METAL 158 Calcium 2 (By similarity).  
 FT METAL 168 Zinc 1 (By similarity).  
 FT METAL 170 Zinc 1 (By similarity).  
 FT METAL 175 Calcium 3 (By similarity).  
 FT METAL 176 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 178 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 180 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 183 Zinc 1 (By similarity).  
 FT METAL 190 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 192 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 194 Calcium 2 (By similarity).  
 FT METAL 196 Zinc 1 (By similarity).  
 FT METAL 198 Calcium 3 (By similarity).  
 FT METAL 199 Calcium 1 (By similarity).  
 FT METAL 201 Calcium 3 (By similarity).  
 FT METAL 218 Zinc 2 (catalytic) (By similarity).  
 FT ACT\_SITE 219 By similarity.  
 FT METAL 222 Zinc 2 (catalytic) (By similarity).  
 FT METAL 228 Zinc 2 (catalytic) (By similarity).  
 FT METAL 285 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 329 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 378 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 427 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT DISULFID 278 466 By similarity.  
 SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;

Query Match 72.3%; Score 222; DB 1; Length 469;  
 Best Local Similarity 70.9%; P-red. No. 9.8e-19;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCGVPDGGFMTGPNKQWERTNLTIRNY 55  
 DB 67 MQRFFGLNVTGKPNBETLDMKKPCGVPDGGFMTGPNKQWERTNLTIRNY 121

RESULT 6

MM01\_HUMAN STANDARD; PRT; 469 AA.

ID MM01\_HUMAN  
 AC P03956; P08156;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (Fibroblast collagenase).  
 DE Name=MMP1; Synonyms=CLG;  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90352587; PubMed=2167156;  
 RX Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A., Stetler-Stevenson W.G.;  
 RA "Cloning and characterization of human tumor cell interstitial collagenase.";  
 RT Cancer Res. 50:5431-5437(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87156645; PubMed=3030290;  
 RX Whittham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,

RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
 RT "Comparison of human stromelysin and collagenase by cloning and  
 RT sequence analysis.",  
 RN Biochem. J. 240:913-916(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86196089; PubMed=3009463;  
 RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,  
 RA Eisen A.Z.;  
 RT "Human fibroblast collagenase. Complete primary structure and homology  
 RT to an oncogene transformation-induced rat protein.",  
 RN J. Biol. Chem. 261:6600-6605(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
 RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
 RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
 RA Heller R., Davis R.W.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Sapetenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whang J., Heiton E., Kretzmer M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Glickman J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 1-35 FROM N.A.  
 RX MEDLINE=87257941; PubMed=3037355;  
 RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,  
 RA Herrlich P.;  
 RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human  
 RT collagenase gene is mediated by an inducible enhancer element located  
 RT in the 5'-flanking region.",  
 RL Mol. Cell. Biol. 7:2256-2266(1987).  
 RN [7]  
 RP SEQUENCE OF 1-70 FROM N.A.  
 RC TISSUE=Synovial cell;  
 RX MEDLINE=87109799; PubMed=3027129;  
 RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;  
 RT "Molecular cloning of human synovial cell collagenase and selection of  
 RT a single gene from genomic DNA.",  
 RL J. Clin. Invest. 79:542-546(1987).  
 RN [8]  
 RP SEQUENCE OF 100-112 AND 270-287.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=90104231; PubMed=2557822;  
 RA Clark I.M., Cawston T.E.;  
 RT "Fragments of human fibroblast collagenase. Purification and  
 RT characterization.",  
 RL Biochem. J. 263:201-206(1989).  
 RN [9]  
 RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.  
 RX MEDLINE=87194799; PubMed=3032950;  
 RA McKerrow J.H.;  
 RT "Human fibroblast collagenase contains an amino acid sequence

RT homologous to the zinc-binding site of Serratia protease.",  
 RL J. Biol. Chem. 262:5943-5943(1987).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.  
 RX MEDLINE=95384760; PubMed=7656013;  
 RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,  
 RA Brown P.A., Johnson W.H., Murray E.J.;  
 RT "Structure of the catalytic domain of human fibroblast collagenase  
 RT complexed with an inhibitor.",  
 RL Nat. Struct. Biol. 1:106-110(1994).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.  
 RX MEDLINE=94304829; PubMed=8031754;  
 RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;  
 RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase  
 RT complexed to itself.",  
 RL Biochemistry 33:8207-8217(1994).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.  
 RX MEDLINE=94105765; PubMed=8278810;  
 RA Lovejoy B., Cleahey A., Hassell A.M., Longley K., Luther M.A.,  
 RA Weigl D., McEneaney G., McElroy A.B., Drewry D., Lambert M.H.,  
 RA Jordan S.R.;  
 RT "Structure of the catalytic domain of fibroblast collagenase complexed  
 RT with an inhibitor.",  
 RL Science 263:375-377(1994).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.  
 RX MEDLINE=94377426; PubMed=8090713;  
 RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks K.J.,  
 RA Johnson J.S., Cook B.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;  
 RT "1.56-A structure of mature truncated human fibroblast collagenase.",  
 RL Proteins 19:98-109(1994).  
 RN [14]  
 RP STRUCTURE BY NMR OF 101-269.  
 RX MEDLINE=98145213; PubMed=9484219;  
 RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,  
 RA Powers R.;  
 RT "High-resolution solution structure of the inhibitor-free catalytic  
 RT fragment of human fibroblast collagenase determined by  
 RT multidimensional NMR.",  
 RL Biochemistry 37:1495-1504(1998).  
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
 CC the helical domain. Also cleaves collagens of types VII and X.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 CC collagen. Cleavage of the triple helix of collagen at about three-  
 CC quarters of the length of the molecule from the N-terminus at  
 CC 775-Gly-1-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 CC substrates and alpha-macroglobulins at bonds where P1' is a  
 CC hydrophobic residue.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
 CC -!- ENZYME REGULATION: Can be activated without removal of the  
 CC activation peptide.  
 CC -!- DOMAIN: There are two distinct domains in this protein; the  
 CC catalytic N-terminal, and the C-terminal which is involved in  
 CC substrate specificity and in binding TIMP (tissue inhibitor of  
 CC metalloproteinases).  
 CC -!- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and  
 CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22  
 CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form  
 CC can act as activator for collagenase.  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X05231; CAA28858.1; -



KW Extracellular matrix: Glycoprotein; Hydrolase; Metal-binding;  
 KW Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 18  
 FT PROPEP 19 99 Activation peptide.  
 FT CHAIN 100 469 Interstitial collagenase.  
 FT DOMAIN 275 469 Hemopexin-like.  
 FT SITE 92 92 Cysteine switch (Potential).  
 FT METAL 124 124 Calcium 1 (By similarity).  
 FT METAL 158 158 Calcium 2 (By similarity).  
 FT METAL 168 168 Zinc 1 (By similarity).  
 FT METAL 170 170 Zinc 1 (By similarity).  
 FT METAL 175 175 Calcium 3 (By similarity).  
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 183 183 Zinc 1 (By similarity).  
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 194 194 Calcium 2 (By similarity).  
 FT METAL 196 196 Zinc 1 (By similarity).  
 FT METAL 198 198 Calcium 3 (By similarity).  
 FT METAL 199 199 Calcium 1 (By similarity).  
 FT METAL 201 201 Calcium 3 (By similarity).  
 FT METAL 218 218 Zinc 2 (catalytic) (By similarity).  
 FT ACT\_SITE 219 219 By similarity.  
 FT METAL 222 222 Zinc 2 (catalytic) (By similarity).  
 FT METAL 228 228 Zinc 2 (catalytic) (By similarity).  
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).  
 FT DISULFID 278 466 By similarity.  
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 22 23 AT -> FP (in Ref. 2).  
 FT CONFLICT 30 30 D -> L (in Ref. 2).  
 FT CONFLICT 35 36 KK -> LL (in Ref. 2).  
 FT CONFLICT 85 85 N -> F (in Ref. 2).  
 FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).  
 FT CONFLICT 113 113 N -> D (in Ref. 2).  
 SQ SEQUENCE 469 AA; B4A5504CE24BD7B5 CRC64;  
 Query Match 71.0%; Score 218; DB 1; Length 469;  
 Best Local Similarity 70.9%; Pred. No. 3.1e-18;  
 Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MQRFGLNVTGKNEETLDMKKPRGCVDSGGFMLTPGNPKWERTNLTYYRINY 55  
 DB 67 MQRFGLRVTKGDAETLNWKKPRGCVDPVAFVLTGKSCWENTNLTYYRINY 121  
 RESULT 9  
 MM01 RANCA STANDARD; PRT; 384 AA.  
 ID MM01 RANCA  
 AC Q1113;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (TC1).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=9400;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=95071832; PubMed=7981043;  
 RA Oofusa K., Yomori S., Yoshizato K.;  
 RT "Regionally and hormonally regulated expression of genes of collagen  
 and collagenase in the anuran larval skin.";  
 RL Int. J. Dev. Biol. 38:345-350(1994).  
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
 the helical domain. Also cleaves preferentially one bond in native  
 collagen. Cleavage of the triple helix of collagen at about three-  
 quarters of the length of the molecule from the N-terminus at  
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 substrates and alpha-macroglobulins at bonds where PI\* is a  
 hydrophobic residue.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By  
 similarity).  
 CC -!- ENZYME REGULATION: Can be activated without removal of the  
 activation peptide (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; S75623; AAB32561.1; -;  
 DR PIR; I51267; I51267.  
 DR HSPF; P21692; IFL.  
 DR MEROPS; M10.001; -;  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; POED-like.  
 DR Pfam; PF00045; Hemopexin; 2.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR SMART; SM00120; HX; 2.  
 DR SMART; SM00235; ZmC; 1.  
 DR PROSITE; PS00546; CYSTEINE SWITCH; FALSE\_NEG.  
 DR PROSITE; PS00024; HEMOPEXIN; FALSE\_NEG.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 DR Calcium-binding; Collagen degradation; Extracellular matrix;  
 KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 25 Potential.  
 FT PROPEP 26 88 Activation peptide (Potential).  
 FT CHAIN 89 384 Interstitial collagenase.  
 FT DOMAIN 239 384 Hemopexin-like.  
 FT SITE 81 81 Cysteine switch (Potential).  
 FT METAL 113 113 Calcium 1 (By similarity).  
 FT METAL 129 129 Calcium 2 (By similarity).  
 FT METAL 139 139 Zinc 1 (By similarity).  
 FT METAL 141 141 Zinc 1 (By similarity).  
 FT METAL 146 146 Calcium 3 (By similarity).  
 FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By similarity).  
 FT METAL 154 154 Zinc 1 (By similarity).  
 FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By similarity).  
 FT METAL 165 165 Calcium 2 (By similarity).  
 FT METAL 167 167 Zinc 1 (By similarity).

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FT METAL 169          Calcium 3 (By similarity).
FT METAL 170          Calcium 1 (By similarity).
FT METAL 172          Calcium 3 (By similarity).
FT METAL 189          Zinc 2 (catalytic) (By similarity).
FT ACT SITE 190          By similarity.
FT METAL 193          Zinc 2 (catalytic) (By similarity).
FT METAL 199          Zinc 2 (catalytic) (By similarity).
FT METAL 249          Calcium 4 (via carbonyl oxygen) (By
FT METAL 277          similarity).
FT METAL 347          Calcium 4 (via carbonyl oxygen) (By
FT METAL 381          similarity).
FT DISULFID 242          Calcium 4 (via carbonyl oxygen) (By
FT SEQUENCE 384 AA; 43582 MW; A5B5E2FB3229DF CRC64;
Query Match 65.5%; Score 201.5; DB 1; Length 384;
Best Local Similarity 65.5%; Pred. No. 2.7e-16;
Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MQRFFGLNTGKPNBETLDMKKPCGVPDSCGFMTPGNPKWERTNLTIRNY 55
Db 57 LKQFFGLKVTGKPDATL-VKQSTCGVDPDVGVEVLTGPNRWENTHLYRIENY 110

RESULT 10
Q8C209 PRELIMINARY; PRT; 465 AA.
ID Q8C209 PRELIMINARY;
AC Q8C209;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone: F73004H20 product: matrix
DE metalloprotease 8, full insert sequence.
GN Names=Mmp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume N.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akanita S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089516; BAC40911.1; -
DR HSP; P22894; IJAP.
DR MGD; MGI:1202395; Mmp8.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR009070; PGED_Like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
DR SEQUENCE 465 AA; 53053 MW; B8BDE6D203712489 CRC64;
Query Match 64.5%; Score 198; DB 2; Length 465;
Best Local Similarity 65.5%; Pred. No. 9e-16;
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY 1 MQRFFGLNTGKPNBETLDMKKPCGVPDSCGFMTPGNPKWERTNLTIRNY 55
Db 66 MQRFFSLAETGKLDAAATMGIMEMPRGVPDSCGDFLLTGPSPKWTHTLTIRINH 120

RESULT 11
Q8C230 PRELIMINARY; PRT; 465 AA.
ID Q8C230 PRELIMINARY;
AC Q8C230;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone: F730018B13 product: matrix
DE metalloprotease 8, full insert sequence.
GN Names=Mmp8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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ID BAC40805 PRELIMINARY; PRT; 465 AA.  
AC BAC40805;  
DT 14-APR-2004 (TEMBLrel. 27, Created)  
DT 14-APR-2004 (TEMBLrel. 27, Last sequence update)  
DT 14-APR-2004 (TEMBLrel. 27, Last annotation update)  
DE NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched  
DE library, clone: F630050H05 product: matrix metalloproteinase 8, full  
DE insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_SEQUENCE FROM N.A.  
RP STRAIN=NOD;  
RC MEDLINE=22354683; PubMed=12466851;  
RX The FANTOM Consortium,  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690 (2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44 (1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771 (2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akanira S., Takeda Y., Tanaka I.,  
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK089234; BAC40805.1; -.  
SQ SEQUENCE 465 AA; 53125 MW; 448AEC59639E9237 CRC64;  
Query Match 64.5%; Score 198; DB 2; Length 465;  
Best Local Similarity 65.5%; Pred. No. 9e-16;  
Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNPKWERNLTYRINY 55  
Db 66 MQRFFSLAETGKLDAAATGMINEMPRCGVDPDSGDFLLTGPSPKWTHTLTYRIINH 120  
RESULT 14  
Q6Y4Q5 PRELIMINARY; PRT; 478 AA.  
ID Q6Y4Q5  
AC Q6Y4Q5;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
DE Stromelysin 1.  
DE Stromelysin 1.  
GN Name=MMP3;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary;  
RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY183143; AA063580.1; -.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_zn\_BS.  
DR Pfam; PF00045; Hemopexin\_4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00138; MATRILIN.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZnMc; 1.  
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;  
Query Match 64.5%; Score 198; DB 2; Length 478;  
Best Local Similarity 63.6%; Pred. No. 9.3e-16;  
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRGCVDPDSGFMLTGPNPKWERNLTYRINY 55  
Db 67 MQRFLGLEVTGKVDSDTLAMRRPRCGVDPVGDFTTFPGMPKWKTHLTYRINY 121  
RESULT 15  
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ID AA063580  
AC AA063580;  
DT 02-MAR-2004 (TEMBLrel. 27, Created)  
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)  
DE Stromelysin 1.  
GN MMP3;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Salivary;  
RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

Search completed: November 15, 2004, 14:06:39  
Job time : 51.7692 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 89.1795 Seconds  
(without alignments)  
189.050 Million cell updates/sec

Title: US-10-032-376A-8  
Perfect score: 258  
Sequence: 1 LQQLSLPBTGELDSATLXA.....VPDLGRFOTFEGDLKWHHN 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP97130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	8	ADQ17091 Human mat
4	258	100.0	432	5	ABP69247 Human pol
5	258	100.0	702	5	ABP69246 Human pol
6	258	100.0	707	2	AA07077 92-KDa hu
7	258	100.0	707	3	AA07077 Matrix me
8	258	100.0	707	4	AA07077 Amino aci
9	258	100.0	707	4	AA07077 Human mat
10	258	100.0	707	4	AA07077 Human mat
11	258	100.0	707	6	ABU56680 Lung canc
12	258	100.0	707	6	ABU56680 Lung canc
13	258	100.0	707	6	ABU56680 Lung canc
14	258	100.0	707	6	ABU56680 Lung canc
15	258	100.0	707	6	ABU56680 Lung canc
16	258	100.0	707	7	ADN39040 Cancer/an
17	258	100.0	707	7	ADN39040 Cancer/an
18	258	100.0	707	8	ADH17067 Human mat
19	258	100.0	707	8	ADH17067 Human mat
20	258	100.0	707	8	ADH17067 Human mat
21	258	100.0	707	8	ADH17067 Human mat
22	258	100.0	707	8	ADH17067 Human mat
23	228	88.4	43	6	ABG76324 Partial s
24	228	88.4	43	6	ABG76324 Partial s
25	228	88.4	43	8	ADQ17099 Human mat

26	213.5	82.8	730	8	ADJ76307 Marker ge
27	150	58.1	171	5	ABG31461 Peptidase
28	141	54.7	54	6	ABP97127 Human mat
29	141	54.7	54	6	ABG76313 Human mat
30	141	54.7	54	8	ADQ17088 Human mat
31	141	54.7	460	1	AA093629 Sequence
32	141	54.7	477	2	AA093629 Human mat
33	141	54.7	477	2	AA093629 Human mat
34	141	54.7	477	2	AA093629 Human mat
35	141	54.7	477	4	AA093629 Human mat
36	141	54.7	477	4	AA093629 Human mat
37	141	54.7	477	5	AA093629 Human mat
38	141	54.7	477	6	AA093629 Human mat
39	141	54.7	477	6	AA093629 Human mat
40	141	54.7	477	6	AA093629 Human mat
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42	141	54.7	477	6	AA093629 Human mat
43	141	54.7	477	6	AA093629 Human mat
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45	141	54.7	477	7	AA093629 Human mat

ALIGNMENTS

RESULT 1  
ABP97130  
ID ABP97130 standard; peptide; 47 AA.  
XX AC ABP97130;  
XX AC  
XX DT 24-JUN-2003 (first entry)  
XX DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.  
XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
XX KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;  
XX KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
XX KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;  
XX KW dermatological; metastatic; non-metastatic; vascularised; heart disease;  
XX KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
XX KW macular degeneration; diabetic retinopathy; cleavage region.  
XX OS Homo sapiens.  
XX PN W02003018748-A2.  
XX PD 06-MAR-2003.  
XX PF 15-AUG-2002; 2002WO-US026319.  
XX PR 16-AUG-2001; 2001US-0312726P.  
XX PR 21-DEC-2001; 2001US-00032376.  
XX PR 21-MAY-2002; 2002US-00153185.  
XX (KIMS ) KIMBERLY-CLARK WORLDWIDE INC.  
XX Quirk S, Weart IF;  
XX WPI; 2003-381408/36.  
XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.  
XX Claim 17; Page 16; 103pp; English.  
XX The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (I) is also useful for treating injuries, including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 XX SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47  
 DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 2  
 ABG76316  
 ID ABG76316 standard; protein; 47 AA.

XX AC ABG76316;

XX DT 10-MAY-2003 (first entry)

XX DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX KW Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;  
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX OS Homo sapiens.

XX PN WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026138.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00023236.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX DR WPI; 2003-289980/28.

XX PT Novel peptide inhibitor of proteinase activity of matrix  
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for  
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.  
 XX  
 XX PS Claim 1; Page 16; 120pp; English.

XX CC The present invention relates to peptide inhibitors of metalloproteinases  
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have  
 CC peptide sequences related to the cleavage regions of the proenzyme forms  
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular  
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin  
 CC development, treating wounds, preventing scarring, improving skin tone,  
 CC reducing wrinkling and for simulating the development of smooth, healthy  
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing  
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs  
 XX  
 XX SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47  
 DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 3  
 ADQ17091  
 ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX DE Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX KW Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;  
 KW human; matrix metalloproteinase; MMP.

XX OS Homo sapiens.

XX PN US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIR/) QUIRK S.

XX PI Malik S, Quirk S;

XX DR WPI; 2004-506456/48.

XX PT Composition used for preventing and treating wrinkles and treating wounds  
 PT comprises peptide having sequence related to matrix metalloproteinase  
 PT proenzyme.

XX PS Example 1; SEQ ID NO 8; 60pp; English.

XX CC The present invention provides peptides and compositions containing such  
 CC peptides that are useful as agents to maintain healthy skin and to  
 CC promote the condition of the skin. The invention is useful for increasing  
 CC the amount of fibronectin in tissue. The invention is also useful for  
 CC encouraging the maintenance and development of healthy skin, preventing  
 CC and treating wrinkles and for treating wounds. The invention acts as  
 CC vulnerary and dermatological agents. The present sequence is human matrix  
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in  
 CC the exemplification of the invention.

XX SQ Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47  
 DB 1 LKQSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGDLKWHHN 47

RESULT 4  
 ABP69247  
 ID ABP69247 standard; protein; 432 AA.

XX AC ABP69247;

XX DT 20-JAN-2003 (first entry)

Human polypeptide SEQ ID NO 1294.

DE XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;  
 KW anti-parkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antiarthritic.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200270539-A2.  
 PN  
 XX  
 XX 12-SEP-2002.  
 PD  
 XX  
 XX 05-MAR-2002; 2002WO-US005095.  
 PF  
 XX  
 XX 05-MAR-2001; 2001US-00799451.  
 PR  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX  
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 PI  
 XX WPI; 2002-759812/82.  
 DR  
 DR N-PSDB; ABZ11463.  
 DR  
 XX New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative,  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
 PT or coagulation disorders.  
 PT  
 XX  
 PS Claim 9; SEQ ID NO 1294; 1012pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-  
 CC ABZ12066) or their mature protein coding portion, active domain coding  
 CC protein or complementary sequences. The polynucleotides are useful for  
 CC identifying expressed genes or for physical mapping of human genome. The  
 CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight  
 CC markers, as a food supplement, for generating antibodies, in medical  
 CC imaging, screening and diagnostic assays and for treating cell-  
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
 CC arthritis, etc. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 432 AA;  
 XX  
 Query Match 100.0%; Score 258; DB 5; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 LQKQLSPETGELDSATLKAMETPCGVPDLGRFOTPEGLKWHHN 47  
 DB 74 LQKQLSPETGELDSATLKAMETPCGVPDLGRFOTPEGLKWHHN 120  
 XX  
 RESULT 5  
 ID ABP69246  
 AC ABP69246;  
 XX  
 XX 20-JAN-2003 (first entry)  
 DT  
 XX

Human polypeptide SEQ ID NO 1293.

DE XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;  
 KW anti-parkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antiarthritic.  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200270539-A2.  
 PN  
 XX  
 XX 12-SEP-2002.  
 PD  
 XX  
 XX 05-MAR-2002; 2002WO-US005095.  
 PF  
 XX  
 XX 05-MAR-2001; 2001US-00799451.  
 PR  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX  
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 PI  
 XX WPI; 2002-759812/82.  
 DR  
 DR N-PSDB; ABZ11463.  
 DR  
 XX New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative,  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
 PT or coagulation disorders.  
 PT  
 XX  
 PS Claim 9; SEQ ID NO 1293; 1012pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-  
 CC ABZ12066) or their mature protein coding portion, active domain coding  
 CC protein or complementary sequences. The polynucleotides are useful for  
 CC identifying expressed genes or for physical mapping of human genome. The  
 CC encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight  
 CC markers, as a food supplement, for generating antibodies, in medical  
 CC imaging, screening and diagnostic assays and for treating cell-  
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
 CC arthritis, etc. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 702 AA;  
 XX  
 Query Match 100.0%; Score 258; DB 5; Length 702;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 LQKQLSPETGELDSATLKAMETPCGVPDLGRFOTPEGLKWHHN 47  
 DB 74 LQKQLSPETGELDSATLKAMETPCGVPDLGRFOTPEGLKWHHN 120  
 XX  
 RESULT 6  
 ID AAR07077  
 AC AAR07077;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 19-FEB-1991 (first entry)  
 XX

XX DE 92-kDa human type IV collagenase gene product.  
 XX KW Epidermal growth factor; EGF; interleukin 1; IL-1; tumour TPA.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT FT 20..707  
 FT FT /label= Mature protein  
 FT FT 38..40  
 FT FT /label= Glycosylation site  
 FT FT 120..122  
 FT FT /label= Glycosylation site  
 FT FT 127..129  
 FT FT /label= Glycosylation site  
 XX EP39859-A.  
 XX 22-NOV-1990.  
 XX PF 14-MAY-1990; 90EP-00870069.  
 XX PR 15-MAY-1989; 89US-00352078.  
 XX (UNITW ) UNIV WASHINGTON.  
 XX PA Goldberg GL, Eisen AZ;  
 XX PI WPI; 1990-350579/47.  
 XX DR N-PSDB; AAQ06554.  
 XX PT New 92-kD type IV collagenase and cDNA - from SV-40 transformed foetal  
 PT lung fibroblasts.  
 XX Claim 4; Fig 3; 2ipp; English.  
 XX SV40 transformed foetal lung fibroblasts may be used to produce type IV  
 CC collagenase, totally glycosylated at three sites. The enzyme is induced  
 CC by EGF, IL-2 and the tumour promoter, 12-O-tetradecanoyl-phorbol acetate  
 CC (TPA) and has therapeutic activity, being able to digest native type IV  
 CC and V collagen. (Updated on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 707 AA;  
 Query Match 100.0%; Score 258; DB 2; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFFGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFFGDLKWHHN 120  
 RESULT 7  
 AAY58015  
 ID AAY58015 standard; protein; 707 AA.  
 XX AC AAY58015;  
 XX DT 28-FEB-2000 (first entry)  
 XX DE Matrix metalloproteinase-9 (MMP-9) amino acid sequence.  
 XX KW Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;  
 KW inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;  
 KW neurological disease; multiple sclerosis; arthritis; human.  
 XX OS Homo sapiens.  
 XX PN WO9957315-A2.  
 XX PD 11-NOV-1999.

XX 07-MAY-1999; 99WO-GB001447.  
 XX 07-MAY-1998; 98GB-00009764.  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX Zhang BP, Ye S, Henney A;  
 XX WPI; 2000-052977/04.  
 XX DR N-PSDB; AA245145.  
 XX PT Detection of matrix metalloproteinase 9 gene polymorphisms for diagnosis or  
 PT prognosis of diseases characterized by metalloproteinase mediated  
 PT remodelling.  
 XX Example 1; Fig 1; 29pp; English.  
 XX This is the human matrix metalloproteinase-9 (MMP-9) amino acid sequence.  
 CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.  
 CC MMP activity is associated with inflammatory diseases and MMP-9 is  
 CC implicated in the pathology of multiple sclerosis. Certain polymorphic  
 CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated  
 CC region of the human MMP-9 gene can affect the severity of  
 CC atherosclerosis. The invention relates to the presence or absence of one  
 CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),  
 CC detection of this polymorphism using oligonucleotides AA245137-245140 can  
 CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T  
 CC polymorphism is a regulatory functional polymorphism. The methods and  
 CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They  
 CC are useful for the diagnosis and prognosis of diseases characterized by  
 CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour  
 CC invasion and metastasis, inflammatory disease, and neurological diseases,  
 CC particularly those involving demyelination such as multiple sclerosis,  
 CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be  
 CC used for screening compounds that bind specifically to a molecule encoded  
 CC by one variant of a polymorphic sequence, thus identifying compounds  
 CC which modulate the activity of the enzyme. Such compounds can then be  
 CC used for rational drug design  
 XX SQ Sequence 707 AA;  
 Query Match 100.0%; Score 258; DB 3; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFFGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFFGDLKWHHN 120  
 RESULT 8  
 AAB84611  
 ID AAB84611 standard; protein; 707 AA.  
 XX AC AAB84611;  
 XX DT 05-SEP-2001 (first entry)  
 XX DE Amino acid sequence of matrix metalloproteinase-9.  
 XX KW Growth factor; protein inhibitor; protease; damaged tissue;  
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;  
 KW granulocyte macrophage colony stimulating factor; GM-CSF; UPA;  
 KW vascular endothelial growth factor; urokinase plasminogen activator;  
 KW dermal ulcer; wound.  
 XX OS Homo sapiens.  
 XX PN WO200149309-A2.



```

XX PD 12-JUL-2001.
XX XX
XX PF 21-DEC-2000; 2000WO-IB001935.
XX PD
XX PF 29-DEC-1999; 99GB-00030768.
XX PR
XX PF (PF12 ) PFIZER LTD.
XX PA (PF12 ) PFIZER INC.
XX XX
XX PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX XX
XX DR WPI; 2001-418351/44.
XX DR N-PSDB; AAH28226.
XX XX
XX PT Composition for the treatment of damaged tissue i.e. chronic wounds and
XX PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX PT factor.
XX XX
XX PS Disclosure; Page 557; 572pp; English.
XX XX
XX CC The specification describes a pharmaceutical composition, comprising a
XX CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
XX CC inhibits the action of at least one specific adverse protein, i.e. a
XX CC protease, that is upregulated in a damaged tissue such as a wound
XX CC environment. Growth factors which are included in the composition of the
XX CC invention are platelet-derived growth factor (PDGF), fibroblast growth
XX CC factor (FGF), connective tissue derived growth factor (CTGF),
XX CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
XX CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
XX CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
XX CC and chrysalin. Inhibitors which are included in the composition of the
XX CC invention include inhibitors of urokinase-type plasminogen activator
XX CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
XX CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
XX CC The present sequence represents a human MMP-9, and is used to produce the
XX CC composition of the invention
XX SQ
XX Sequence 707 AA;

Query Match 100.0%; Score 258; DB 4; Length 707;
Best Local Similarity 100.0%; Pred. No. 8.7e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 9
AAE10432
ID AAE10432 standard; protein; 707 AA.
XX AC
XX AC AAE10432;
XX DT 10-DEC-2001 (first entry)
XX DE Human matrix metalloproteinase-9 (MMP-9) protein.
XX KW Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide 1..21
XX FT /label= Signal_peptide
XX FT Protein 22..707
XX FT /label= Mature_MMP_2_protein
XX FT Domain 97..103
XX FT /label= Cysteine_switch_domain
XX FT 168..192
XX FT /note= "Zinc and calcium binding domain"

```

WO200166766-A2.  
 13-SEP-2001.  
 06-MAR-2001; 2001WO-US007167.  
 06-MAR-2000; 2000US-0187196P.  
 (DARW-) DARWIN MOLECULAR CORP.  
 (SCHA/) SCHATZMAN R.  
 Fajardo M, Wang K, Smith R, Moss P;  
 WPI; 2001-582276/65.  
 Novel isolated matrix metalloproteinase-25 nucleic acid molecule and  
 proteins encoded by them whose inhibition is useful for modulation of  
 hair growth in mammals.  
 Example 2; Fig 3; 119pp; English.  
 The present sequence is human matrix metalloproteinase (MMP)-9 protein.  
 used in the exemplification of the invention. MMP-25 DNA is located on  
 chromosome 11q22. Matrix metalloproteinases are a family of zinc  
 dependent endopeptidases that function extracellularly to degrade  
 proteins typically found in the extracellular matrix. MMP-25 is expressed  
 in skin cells of mammals, particularly in breast cells and hair  
 follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule  
 encoding all or part of MMP by hybridising MMP-25 to a nucleic acid  
 sample and identifying a sequence that hybridises in the nucleic acid  
 sample. The identification step involves performing polymerase chain  
 reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is  
 useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used  
 to modulate hair growth and breast cancer in a mammal

Query Match 100.0%; Score 258; DB 4; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47  
 Db 74 LQQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 10  
 AAB20491  
 ID AAB20491 standard; protein; 707 AA.  
 XX AC  
 XX AC AAB20491;  
 XX DT 21-JUN-2001 (first entry)  
 XX DE Human matrix metalloproteinase-9 (MMP-9).  
 XX KW Matrix metalloproteinase-9; MMP-9; human; pain; analgesic;  
 XX KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;  
 XX KW cerebral ischaemia; cerebral infarction; narcotic tolerance;  
 XX KW narcotic withdrawal.  
 XX OS Homo sapiens.  
 XX FH Key  
 XX FT Peptide 1..21  
 XX FT /label= Signal\_peptide  
 XX FT Protein 22..707  
 XX FT /label= Mature\_MMP\_2\_protein  
 XX FT Domain 97..103  
 XX FT /label= Cysteine\_switch\_domain  
 XX FT 168..192  
 XX FT /note= "Zinc and calcium binding domain"



PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-0334370P.  
PR 12-APR-2002; 2002US-0372246P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX  
XX Aziz N, Murray R;  
XX WPI; 2003-093161/08.  
XX N-PSDB; ABX76189.  
XX  
XX Detecting a lung cancer-associated transcript in a cell from a patient  
XX for treating lung cancer, by contacting a biological sample from the  
XX patient with a polynucleotide that exhibits increased or decreased  
XX expression in lung cancer.  
XX  
XX  
XX Claim 27; Page 236; 453pp; English.  
XX  
XX The invention relates to a method for detecting a lung cancer-associated  
XX transcript in a cell from a patient, comprising contacting a biological  
XX sample from the patient with a polynucleotide that selectively hybridizes  
XX to a sequence that is at least 80 % identical to a gene that exhibits  
XX increased or decreased expression in lung cancer samples. Lung cancer-  
XX associated polynucleotides and polypeptides are used for identifying a  
XX compound that modulates a lung cancer-associated polypeptide, for  
XX inhibiting proliferation of a lung cancer-associated cell to treat lung  
XX cancer in a patient and for treating a mammal having lung cancer by  
XX administering a modulatory compound identified. The methods are useful  
XX for treating lung cancer, such as small cell lung cancer, non-small cell  
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful  
XX for diagnostic purposes and as targets for screening for therapeutic  
XX compounds that modulate lung cancer, such as antibodies. Sequences  
XX ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
XX invention  
XX  
XX Sequence 707 AA;  
XX  
XX Query Match 100.0%; Score 258; DB 6; Length 707;  
XX Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 LQKQLSPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47  
XX 74 LQKQLSPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120  
XX  
XX Db  
XX  
XX RESULT 13  
XX AAO16609  
XX ID AAO16609 standard; protein; 707 AA.  
XX AC AAO16609;  
XX XX  
XX DT 08-MAY-2003 (first entry)  
XX DE Human matrix metalloproteinase 9 (MMP9) gelatinase protein.  
XX KW Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;  
XX gelatinase; metalloproteinase mediated disease; drug design; arthritis;  
XX three-dimensional structure; MMP9 inhibitor; tumour growth;  
XX cancer metastasis; osteoarthritis; atherosclerosis; restenosis;  
XX periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;  
XX Graft-versus-host disease; non-insulin dependent diabetes.  
XX KW Homo sapiens.  
XX OS  
XX WO2003002729-A1.  
XX PN  
XX XX 09-JAN-2003.  
XX PD  
XX XX

PF 24-JUN-2002; 2002WO-SE001266.  
XX  
XX 27-JUN-2001; 2001SE-00002298.  
XX  
XX (ASTR ) ASTRAZENECA AB.  
XX  
XX Jepsen H, Minshull C, Paupit R, Rowsell S;  
XX WPI; 2003-201502/19.  
XX  
XX Novel crystalline form of a polypeptide corresponding to the catalytic  
XX domain of matrix metalloproteinase 9 protein, useful for selecting or  
XX designing chemical modulators which are used for treating diabetes,  
XX cancer, arthritis.  
XX  
XX Disclosure; Fig 7; 227pp; English.  
XX  
XX The invention comprises a crystalline form of a polypeptide corresponding  
XX to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a  
XX gelatinase. The crystalline polypeptide of the invention is useful for  
XX treating a metalloproteinase mediated disease or condition in a warm-  
XX blooded animal. The crystalline polypeptide is also useful for  
XX determining the three-dimensional structure of the MMP9 catalytic domain  
XX to high resolution. The three-dimensional structure of the MMP9 catalytic  
XX domain is useful for rational drug design, and the atomic coordinates of  
XX the catalytic domain of MMP9 are useful for selecting or designing  
XX chemical modulators (preferably inhibitors) of MMP9. The crystalline  
XX polypeptide of the invention is useful in the treatment of a  
XX metalloproteinase mediated disease or condition, such as: tumour growth;  
XX metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;  
XX restenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-  
XX versus-host disease; and non-insulin dependent diabetes. The present  
XX amino acid sequence represents a human matrix metalloproteinase 9 (MMP9)  
XX protein  
XX  
XX Sequence 707 AA;  
XX  
XX Query Match 100.0%; Score 258; DB 6; Length 707;  
XX Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 LQKQLSPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47  
XX 74 LQKQLSPETGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120  
XX  
XX Db  
XX  
XX RESULT 14  
XX ABR92116  
XX ID ABR92116 standard; protein; 707 AA.  
XX AC ABR92116;  
XX XX  
XX DT 10-SEP-2003 (first entry)  
XX DE Human cervical cancer cell marker protein SEQ ID NO:142.  
XX KW Human; cervical cancer; cervical cancer marker; cancer therapy;  
XX detection; gene therapy; vaccine.  
XX XX  
XX OS Homo sapiens.  
XX XX  
XX WO2002101075-A2.  
XX PN  
XX PD 19-DEC-2002.  
XX XX  
XX 12-JUN-2002; 2002WO-US018639.  
XX PF  
XX 13-JUN-2001; 2001US-0298155P.  
XX PR  
XX 13-JUN-2001; 2001US-0298159P.  
XX PR  
XX 14-NOV-2001; 2001US-0335936P.  
XX PR  
XX (MILL-) MILLENNIUM PHARM INC.  
XX PA  
XX XX

PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;  
 PI Gannavarapu M, Glatt K, Hoersch S;  
 XX WPI; 2003-156967/15.  
 DR N-PSDB; ACF12899.

XX New isolated nucleic acid molecule useful for detecting, characterizing,  
 PT preventing and treating human cervical cancers, in various prognostic and  
 PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.

XX Claim 4; Page 294-295; 386pp; English.

XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)  
 CC given in ABR92047 to ABR92164. A higher level of expression of (I) than  
 CC normal indicates the presence of cervical cancer. Also described: (1) a  
 CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)  
 CC assessing (M1) whether a patient is afflicted with cervical cancer,  
 CC comprising comparing the level of expression of a marker in a patient's  
 CC sample, and the normal level of expression of the marker in a control non  
 CC -cervical cancer sample, where a significant increase in the level of  
 CC expression of the marker in the patient's sample relative to that in the  
 CC control sample is an indication that the patient is afflicted with  
 CC cervical cancer. (I) has cytostatic activity, and can be used in gene  
 CC therapy and in vaccines. (I) is useful in detecting, characterizing,  
 CC preventing and treating human cervical cancers. (I) may also be used in  
 CC various prognostic and diagnostic assays, pharmacogenomics and in  
 CC monitoring clinical trials

XX Sequence 707 AA;

Query Match 100.0%; Score 258; DB 6; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 47  
 DB 74 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 120

RESULT 15

ADL14993  
 ID ADL14993 standard; protein; 707 AA.

XX ADL14993;

XX 06-MAY-2004 (first entry)

XX Human type IV collagenase protein for cancer treatment.

XX cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;  
 XX prognosis; mantle cell lymphoma; cancer.

XX Homo sapiens.

XX WO2003068268-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-EP001461.

XX 14-FEB-2002; 2002GB-00003480.

XX 29-JUN-2002; 2002GB-00015095.

XX (BIOI-) BIOINVENT INT AB.

XX Ek S, Borrebaeck CAK, Ehinger M;

XX WPI; 2003-697496/66.

XX N-PSDB; ADL14994.

XX New compound for treating, imaging, diagnosing or prognosing mantle cell  
 PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a  
 PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.

PT nucleic acid).  
 XX Disclosure; SEQ ID NO 5; 342pp; English.

XX The invention relates to a compound comprising a binding moiety which  
 CC selectively binds to a protein or polypeptide listed in the specification  
 CC (e.g. human autotaxin polypeptide or human CD24 signal transducer  
 CC polypeptide), and a further moiety. The compound is useful in medicine or  
 CC in the treatment, imaging, diagnosis or prognosis of mantle cell  
 CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a  
 CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells  
 CC in the body of an individual. This sequence corresponds to one of the  
 XX polypeptides of the invention.

XX Sequence 707 AA;

Query Match 100.0%; Score 258; DB 7; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-28;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 47  
 DB 74 LOKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTTFEGDLKWHHN 120

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 Job time : 92.1795 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:02:10 ; Search time 22.2949 Seconds  
(without alignments)  
139.806 Million cell updates/sec

Title: US-10-032-376A-8  
Perfect score: 258  
Sequence: 1 LQKQLSLPETGELDSATLKA.....VPLDGRFQTPEGDLKWHHNN 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	707	3	US-08-704-711A-19
2	258	100.0	707	3	US-09-521-220-19
3	258	100.0	707	3	US-09-391-104-20
4	258	100.0	708	3	US-08-448-489-16
5	141	54.7	477	3	US-08-704-711A-20
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9	141	54.7	477	3	US-09-391-104-21
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11	133	51.6	476	3	US-08-448-489-14
12	133	51.6	476	3	US-09-521-220-21
13	133	51.6	476	3	US-09-391-104-22
14	117	45.3	471	3	US-09-391-104-25
15	115	44.6	136	4	US-09-513-999C-4639
16	115	44.6	663	4	US-09-194-468A-30
17	114	44.2	631	3	US-08-448-489-17
18	114	44.2	660	3	US-08-704-711A-18
19	114	44.2	660	3	US-09-521-220-18
20	114	44.2	660	3	US-09-391-104-19
21	114	44.2	660	4	US-09-917-254-89
22	113	43.8	470	3	US-08-068-392-2
23	113	43.8	470	3	US-08-396-988-2
24	113	43.8	470	3	US-09-391-104-26
25	110	42.6	469	3	US-08-704-711A-16
26	110	42.6	469	3	US-08-448-489-12
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28	110	42.6	469	3	US-09-391-104-23	Sequence 23, Appl
29	109	42.2	513	4	US-10-140-002-192	Sequence 192, App
30	109	42.2	513	4	US-09-862-631-4	Sequence 4, Appli
31	108	41.9	471	4	US-08-994-689C-1	Sequence 1, Appli
32	107	41.5	135	4	US-09-513-999C-4163	Sequence 4163, Ap
33	106	41.1	267	3	US-08-448-489-18	Sequence 18, Appl
34	106	41.1	267	3	US-09-391-104-27	Sequence 27, Appl
35	106	41.1	271	3	US-08-896-062-2	Sequence 2, Appli
36	105	40.7	264	3	US-09-009-156-6	Sequence 6, Appli
37	105	40.7	264	3	US-09-372-154-6	Sequence 6, Appli
38	101	39.1	471	4	US-08-994-689C-21	Sequence 21, Appl
39	100.5	39.0	582	3	US-08-704-711A-2	Sequence 2, Appli
40	100.5	39.0	582	3	US-08-448-489-1	Sequence 1, Appli
41	100.5	39.0	582	3	US-09-211-704A-9	Sequence 9, Appli
42	100.5	39.0	582	3	US-09-521-220-2	Sequence 2, Appli
43	100.5	39.0	582	3	US-09-391-104-28	Sequence 28, Appl
44	100.5	39.0	582	4	US-09-919-497-84	Sequence 84, Appl
45	100	38.8	444	1	US-09-178-002-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-704-711A-19  
; Sequence 19, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/704,711A  
; FILING DATE: 20-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DE95/00357  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 707 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-704-711A-19

us-10-032-376a-8.ra1

Mon Nov 15 13:54:00 2004

Query Match 100.0%; Score 258; DB 3; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
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 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 2  
 US-09-521-220-19  
 ; Sequence 19, Application US/09521220  
 ; Patent No. 6399348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; OF SEQUENCES: 22  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/521,220  
 ; FILING DATE: 08-Mar-2000  
 ; CLASSIFICATION: <Unknown>  
 ; 21-OCT-1994  
 ; 17-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/704,711  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: DE 4438838.1  
 ; FILING DATE: 21-OCT-1994  
 ; APPLICATION NUMBER: DE 4409663.1  
 ; FILING DATE: 17-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GRANADOS, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 26083/124  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 707 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-521-220-19  
 Query Match 100.0%; Score 258; DB 3; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 3  
 US-09-391-104-20  
 ; Sequence 19, Application US/09521220  
 ; Patent No. 6399348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; OF SEQUENCES: 22  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/521,220  
 ; FILING DATE: 08-Mar-2000  
 ; CLASSIFICATION: <Unknown>  
 ; 21-OCT-1994  
 ; 17-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/704,711  
 ; FILING DATE: <Unknown>  
 ; APPLICATION NUMBER: DE 4438838.1  
 ; FILING DATE: 21-OCT-1994  
 ; APPLICATION NUMBER: DE 4409663.1  
 ; FILING DATE: 17-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GRANADOS, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 26083/124  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 707 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-391-104-20  
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 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 4  
 US-08-448-489-16  
 ; Sequence 16, Application US/08448489  
 ; Patent No. 6184022  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SEIKI, Motoharu  
 ; APPLICANT: SAITO, Hiroshi  
 ; APPLICANT: SHINAGAWA, Akira  
 ; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
 ; FILE REFERENCE: 55-290P  
 ; CURRENT APPLICATION NUMBER: US/08/448,489  
 ; CURRENT FILING DATE: 1995-06-07  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 16  
 ; LENGTH: 708  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: X = UNKNOWN  
 ; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
 ; OTHER INFORMATION: Matrix Metalloproteinase Family  
 ; US-08-448-489-16

US-08-448-489-16  
 Query Match 100.0%; Score 258; DB 3; Length 708;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 5  
 US-08-704-711A-20  
 ; Sequence 20, Application US/08704711A  
 ; Patent No. 6114159  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WILL, Horst  
 ; APPLICANT: HINZMANN, Bernd

US-08-704-711A-20  
 Query Match 100.0%; Score 258; DB 3; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47  
 DB 74 LKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 120

RESULT 6  
 US-09-391-104-20  
 ; Sequence 19, Application US/09521220  
 ; Patent No. 6399348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HINZMANN, Bernd

US-09-391-104-20  
 Query Match 100.0%; Score 258; DB 3; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-29;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-15

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Best Local Similarity 62.8%; Pred No. 2.4e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db :|||:|||:|||:|||:|||:|||:|||:|||:|||
   67 MQKFGLGVTKLSDTLEVNRPKRCGVPDVGHFRTPPGIPKW 109

RESULT 7
US-08-281-313-1
; Sequence 9, Application US/09368169
; Patent NO. 6284511
; GENERAL INFORMATION:
; APPLICANT: Tetsuya INAKA et al.
; TITLE OF INVENTION: HEAT-STABLE PROLYENDOPEPTIDASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wengeroth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,169
; FILING DATE: August 5, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/750,816
; FILING DATE: January 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 99-0868/LC(WMC)49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Flavobacterium meningosepticum
; ORGANISM: Mat Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Ala Val Ala V
; ORGANISM: 1
; Sequence 1, Application US/08281313
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Baragi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
ORGANAL SOURCE:  
ORGANISM: Flavobacterium meningosepticum  
ORGANISM: Met Lys Tyr Asn Lys Ser Val Ala Val Ala Phe Ala Val  
ORGANISM: 1  
Sequence 1, Application US/08281313  
Patent No. 6284513  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhuang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
APPLICANT: Baragi, Vijaykumar  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Stromelysin Catalytic Domain Protein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI

COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/281,313  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,705  
FILING DATE: 03-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Tinney, Francis J.  
REGISTRATION NUMBER: 33,069  
REFERENCE/DOCKET NUMBER: 4415-01-FJT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 100..273  
OTHER INFORMATION: /note= "Mature stromelysin"  
OTHER INFORMATION: catalytic domain protein"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..17  
OTHER INFORMATION: /note= "Signal peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 18..99  
OTHER INFORMATION: /note= "Propeptide"  
US-08-281-313-1  
Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
QY 1 LOKQLSLPETGELDSATLKAMETPCGVPDLGRFQTPEGDLKW 43  
DB 67 MQKFLGLEVTGKLDSDTLEVMKPCRGVPDVGHFRTFFGIPKW 109  
RESULT 8  
US-09-521-220-20  
Sequence 20, Application US/09521220  
Patent No. 6399348  
GENERAL INFORMATION:  
APPLICANT: WILL, Horst  
HINZMANN, Bernd  
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/521,220  
FILING DATE: 08-Mar-2000  
CLASSIFICATION: <Unknown>  
21-OCT-1994  
17-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/704,711  
FILING DATE: <Unknown>  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-521-220-20  
Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
QY 1 LOKQLSLPETGELDSATLKAMETPCGVPDLGRFQTPEGDLKW 43  
DB 67 MQKFLGLEVTGKLDSDTLEVMKPCRGVPDVGHFRTFFGIPKW 109  
RESULT 9  
US-09-391-104-21  
Sequence 21, Application US/09391104  
Patent No. 6399371  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Falduto, Michael T.  
APPLICANT: Magnuson, Scott R.  
APPLICANT: Morgan, Douglas W.  
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
TITLE OF INVENTION: OF USING SAME  
FILE REFERENCE: 6073.US.P1  
CURRENT APPLICATION NUMBER: US/09/391,104  
CURRENT FILING DATE: 1999-09-07  
PRIOR APPLICATION NUMBER: US 08/814,394  
PRIOR FILING DATE: 1997-03-11  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 477  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-391-104-21  
Query Match 54.7%; Score 141; DB 3; Length 477;  
Best Local Similarity 62.8%; Pred. No. 2.4e-12;  
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
QY 1 LOKQLSLPETGELDSATLKAMETPCGVPDLGRFQTPEGDLKW 43  
DB 67 MQKFLGLEVTGKLDSDTLEVMKPCRGVPDVGHFRTFFGIPKW 109



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RESULT 10
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCES/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-21
Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LKQLSLPETGELDSATLKAMETPCGVPDLAGRFOTFEGDLKW 43
;
Db 66 MOKFLGLEVTGKLDITLTVMKRRCGVPDVGHFSSFGMPKW 108
;

RESULT 11
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07

US-08-704-711A-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14
Query Match 51.6%; Score 133; DB 3; Length 476;
Best Local Similarity 58.1%; Pred. No. 3.6e-11;
Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 LKQLSLPETGELDSATLKAMETPCGVPDLAGRFOTFEGDLKW 43
;
Db 66 MOKFLGLEVTGKLDITLTVMKRRCGVPDVGHFSSFGMPKW 108
;

RESULT 12
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6393348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCES/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-521-220-21
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21
Query Match 51.6%; Score 133; DB 3; Length 476;
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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 80
; OTHER INFORMATION: Xaa=Lys or Asn or Arg or Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 88
; OTHER INFORMATION: Xaa=Ala or Cys or Phe or Gly or His or Ile or Leu or Asn
; OTHER INFORMATION: Tyr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 104
; OTHER INFORMATION: Xaa=Ala or Pro
US-09-513-999C-4639

Query Match      44.6%; Score 115; DB 4; Length 136;
Best Local Similarity 46.5%; Pred. No. 3.4e-09;
Matches 20; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPDLGRQTTFEGDLKW 43
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 77 MOKFGLPQTGDLNDONTIXXMRKPRCGXPDVAXYNFFPRXXK 119
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Search completed: October 13, 2004, 15:17:04  
Job time : 23.2949 secs

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; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 3
US-10-219-561-8
; Sequence 8, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 4
US-10-032-376A-8
; Sequence 8, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
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; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 5
US-10-335-207-8
; Sequence 8, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47

RESULT 6
US-09-391-104-20
; Sequence 20, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Raldueto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-20

Query Match      100.0%; Score 258; DB 9; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
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Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQQLSLPTGGLDLSATLKAMRPRCGVPDLGRFQTFEGDLKWHHN 47
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Db 74 LQQLSLPTGGLDLSATLKAMRPRCGVPDLGRFQTFEGDLKWHHN 120

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RESULT 9
US-10-301-822-132
; Sequence 132, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Subhang
; APPLICANT: Schlegel, Robert
; APPLICANT: Morahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 707

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US-10-301-822-132

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. NO. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOKQLSLPETGELDSATLKAAMTPTCGVPLGRFQTPEGDLKWHHN 47
        |||.....|.....|.....|.....|.....|.....|
Db       74 LQKQLSLPETGELDSATLKAAMTPTCGVPLGRFQTPEGDLKWHHN 120
        |||.....|.....|.....|.....|.....|.....|

RESULT 10
US-10-131-985-33
; Sequence 33, Application US/10131985
; Publication No. US2003019940A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: McClellon, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 707
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-131-985-33

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQKQLSLPTGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 11
US-10-295-027-358
; Sequence 358, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1253
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1253

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 47
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Db 74 LQKQLSLPTGELDSATLKAMTRPCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 13
US-10-440-464-66
; Sequence 66, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRINO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
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; PRIOR APPLICATION NUMBER: 60/380,872  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/448,922  
; PRIOR FILING DATE: 2003-02-24  
; PRIOR APPLICATION NUMBER: 60/448,874  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 66  
; LENGTH: 707  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-440-464-66

Query Match 100.0%; Score 258; DB 15; Length 707;  
Best Local Similarity 100.0%; Pred. No. 2.2e-26;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47  
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

## RESULT 14

US-10-447-315-7  
; Sequence 7, Application US/10447315  
; Publication No. US20040071687A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafii, Shahin  
; APPLICANT: Heissig, Beate  
; APPLICANT: Hattori, Koichi  
; APPLICANT: Cornell Research Foundation, Inc.  
; TITLE OF INVENTION: Adult Stem Cell Recruitment  
; FILE REFERENCE: 1676.006US1  
; CURRENT APPLICATION NUMBER: US/10/447,315  
; PRIOR FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: US 60/383,658  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 707  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-447-315-7

Query Match 100.0%; Score 258; DB 15; Length 707;  
Best Local Similarity 100.0%; Pred. No. 2.2e-26;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47  
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

## RESULT 15

US-10-480-621-2  
; Sequence 2, Application US/10480621  
; Publication No. US20040175817A1  
; GENERAL INFORMATION:  
; APPLICANT: Jepson, Holly  
; APPLICANT: Minshull, Claire  
; APPLICANT: Paupit, Richard  
; APPLICANT: Rowse, Sian  
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX  
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF  
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN  
; TITLE OF INVENTION: MMP9 MODULATORS  
; FILE REFERENCE: 06275-377US1  
; CURRENT APPLICATION NUMBER: US/10/480,621  
; PRIOR FILING DATE: 2003-12-12  
; PRIOR APPLICATION NUMBER: PCT/SE02/01266  
; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: SE 0102298-7  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 707  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-480-621-2

Query Match 100.0%; Score 258; DB 16; Length 707;  
Best Local Similarity 100.0%; Pred. No. 2.2e-26;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47  
DB 74 LQKQLSPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

Search completed: October 13, 2004, 15:35:39  
Job time : 66.8846 secs

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A:Molecule type: protein  
 A:Residues: 20-25,'X','27-37 <VNS>  
 A:Experimental source: monocytic cell line THP-1  
 A>Note: sequence extracted from NCBI backbone (NCBI:63812) and corrected to correspond  
 R:Opdenakker, G.; Masure, S.; Grillet, B.; Van Damme, J.  
 A:Title: Cytokine-mediated regulation of human leukocyte gelatinases and role in arthritis  
 A:Reference number: A61385; MUID:92032113; PMID:1932376  
 A:Accession: A61385  
 A:Molecule type: protein  
 A:Residues: 28-37 <OPD>  
 R:Masure, S.; Proost, P.; van Damme, J.; Opdenakker, G.  
 Eur. J. Biochem. 198, 391-398, 1991  
 A:Title: Purification and identification of 91-kDa neutrophil gelatinase. Release by the  
 A:Reference number: S16097; MUID:91249834; PMID:1645657  
 A:Accession: S16097  
 A:Molecule type: protein  
 A:Residues: 28-42,'X','44-60,'XX','63 <WAS>  
 R:Sang, O.X.; Birkedal-Hansen, H.; van Wart, H.E.  
 Biochim. Biophys. Acta 1251, 99-108, 1995  
 A:Title: Proteolytic and non-proteolytic activation of human neutrophil progelatinase B.  
 A:Reference number: S59488; MUID:95399447; PMID:7669817  
 A:Accession: S59488  
 A:Molecule type: protein  
 A:Residues: 20-27;60-87;94-98,'X','100-101,107-114 <SAS>  
 A:Comment: Gelatinase B hydrolyzes peptide bonds in plasminogen to yield a fragment with  
 C:Genetics:  
 A:Gene: GDB:MPP9; CLG4B  
 A:Cross-references: GDB:125224; OMIM:120361  
 A:Map position: 20c12-20q13  
 A:Introns: 46/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 537/2; 584/1; 634/2; 6  
 C:Function:  
 A:Description: hydrolyzes type IV collagen  
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:20-707/Product: gelatinase B proenzyme #status predicted <PRE>  
 F:20-106/Domain: activation peptide #status predicted <ACT>  
 F:28-707/Product: 91K neutrophil gelatinase B proenzyme #status predicted <PR>  
 F:107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>  
 F:230-273/Domain: fibronectin type II repeat homology <2F9>  
 F:288-329/Domain: fibronectin type II repeat homology <2F8>  
 F:347-388/Domain: fibronectin type II repeat homology <2F1>  
 F:445-497/Region: proline-rich  
 F:509-704/Domain: hemopexin repeat homology <PXN>  
 F:38,120,127/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted  
 F:402/Active site: Glu #status predicted  
 Query Match 100.0%; Score 258; DB 1; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 47  
 DB 74 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 120  
 RESULT 2  
 JC4364  
 Gelatinase B (EC 3.4.24.35) precursor - rat  
 N:Alternate names: 92-kDa type IV collagenase; matrix metalloproteinase 9 (MMP9)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Jan-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
 A:Accession: JC4364  
 R:Okada, A.; Santavirta, M.; Basset, P.  
 Gene 164, 317-321, 1995  
 A:Title: The cDNA cloning and expression of the gene encoding rat gelatinase B.  
 A:Reference number: JC4364; MUID:96069602; PMID:7590350  
 A:Accession: JC4364  
 A:Molecule type: mRNA  
 A:Residues: 1-708 <OKA>

A:Cross-references: UNIPROT:P50282; GB:U24441; NID:91173505; PIDN:AAA90911.1; PID:911735  
 A:Experimental source: skin wounds  
 C:Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzym  
 ogression.  
 C:Genetics:  
 A:Gene: galb  
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol  
 C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-708/Product: progelatinase B #status predicted <PRO>  
 F:25-107/Domain: activation peptide #status predicted <ACT>  
 F:108-708/Product: gelatinase B #status predicted <MAT>  
 F:214-389/Region: collagen binding #status predicted  
 F:231-272/Domain: fibronectin type II repeat homology <2F1>  
 F:289-330/Domain: fibronectin type II repeat homology <2F2>  
 F:348-389/Domain: fibronectin type II repeat homology <2F3>  
 F:514-707/Domain: hemopexin repeat homology <PXN>  
 F:39,121/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted  
 F:403/Active site: Glu #status predicted  
 F:519-707/Disulfide bonds: #status predicted  
 Query Match 91.5%; Score 236; DB 2; Length 708;  
 Best Local Similarity 87.2%; Pred. No. 1.6e-23;  
 Matches 41; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 47  
 DB 75 LQKQSLPPTGELDSATLKAMTPRCGVDPDLGRFOTFGDLKWHHN 121  
 RESULT 3  
 A53796  
 Gelatinase B (EC 3.4.24.35) precursor - rabbit  
 N:Alternate names: 92K matrix metalloproteinase; 92K type IV collagenase; matrix metallo  
 C:Species: Oryctolagus cuniculus (Domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: A53796; A55398  
 R:Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Eg  
 J. Biol. Chem. 269, 15006-15009, 1994  
 A:Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.  
 A:Reference number: A53796; MUID:94253056; PMID:8195136  
 A:Accession: A53796  
 A:Molecule type: mRNA  
 A:Residues: 1-707 <TEZ>  
 A:Cross-references: UNIPROT:P41246; GB:D26514; NID:G499372; PIDN:BAA05520.1; PID:G499373  
 A:Experimental source: osteoclasts  
 R:Finzi, M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Mody, M.K.; Girard, M.T.; R  
 J. Biol. Chem. 269, 28620-28628, 1994  
 A:Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of API and AP2 in cel  
 A:Reference number: A55398; MUID:95050662; PMID:7961810  
 A:Accession: A55398  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-75,'P','77-99,'ASR','103-171 <FIN>  
 A:Cross-references: GB:U36050; NID:9535714; PIDN:AAA64358.1; PID:9535715  
 C:Genetics:  
 A:Introns: 46/3; 124/2  
 C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol  
 C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-106/Domain: activation peptide #status predicted <ACT>  
 F:107-707/Product: 91K neutrophil gelatinase B #status predicted <PRO>  
 F:230-271/Domain: fibronectin type II repeat homology <2F9>  
 F:288-329/Domain: fibronectin type II repeat homology <2F8>  
 F:347-388/Domain: fibronectin type II repeat homology <2F1>  
 F:510-704/Domain: hemopexin repeat homology <PXN>  
 F:88,120,127/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted  
 F:402/Active site: Glu #status predicted

```

Query Match          91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 2.2e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELSDATLKAMRPRCGVPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 74 LQKLSLPETGELSDATLEAMRPRCGVPDVGKQTFEGDLKWHHN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Gelatinase B (EC 3.4.24.35) precursor - rat
N:Alternate names: collagenase type IV
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62907; S72371
R:Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 382, 285-288, 1996
A:Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinant
A:Reference number: S62907; MUID:96184505; PMID:8605986
A:Accession: S62907
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-708 <XIA>
A:Cross-references: UNIPROT:P50282; EMBL:U36476
R:Feng, L.
submitted to the EMBL Data Library, September 1995
A:Reference number: S72371
A:Accession: S72371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-127, 'S', 129-708 <FEN>
A:Cross-references: EMBL:U36476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784
C:Superfamily: Gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-107/Domain: propeptide #status predicted <PRO>
F:25-107/Domain: activation peptide #status predicted <ACT>
F:68-217,393-445/Domain: matrix metalloproteinase homology #status atypical <MAP>
F:108-708/Product: gelatinase A #status predicted <MAT>
F:214-389/Region: collagen binding #status predicted
F:231-272/Domain: fibronectin type II repeat homology <2F1>
F:289-330/Domain: fibronectin type II repeat homology <2F2>
F:348-389/Domain: fibronectin type II repeat homology <2F3>
F:514-707/Domain: hemopexin repeat homology <PXM>
F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F:403/Active site: Glu #status predicted
F:519-707/Disulfide bonds: #status predicted

Query Match          90.3%; Score 233; DB 2; Length 708;
Best Local Similarity 85.1%; Pred. No. 4.2e-23;
Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELSDATLKAMRPRCGVPDLGRFQTFEGDLKWHHN 47
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 LQKLSLPETGELSDATLEAMRPRCGVPDVGKQTFEGDLKWHHN 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
I46031
Gelatinase B (EC 3.4.24.35) - bovine
N:Alternate names: matrix metalloproteinase 9 (MMP9)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46031; S43112
R:Baylis, H.A.; Megson, A.; Hall, R.
Mol. Biochem. Parasitol. 69, 211-222, 1995
A:Title: Infection with Thelazia annulata induces expression of matrix metalloproteinases
A:Reference number: I46031; MUID:95287902; PMID:7770085
A:Accession: I46031
A:Status: translated from GS/EMBL/DDJB
A:Molecule type: mRNA

```

A;Residues: 1-730 <TAN>  
A;Cross-references: UNIPROT:P41245; DDBJ:D12712; NID:G286079; PIDN:BA02208.1; PID:G2860  
R;Masure, S.; Nys, G.; Fiten, P.; van Damme, J.; Opendakker, G.  
Eur. J. Biochem. 218, 129-141, 1993  
A;Title: Mouse gelatinase B. cDNA cloning, regulation of expression and glycosylation in  
A;Reference number: S39525; MUID:94062823; PMID:8243459  
A;Accession: S39525  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-638, 'L', '640-730 <MAS>  
A;Cross-references: EMBL:X72794; NID:G433432; PIDN:CAA51314.1; PID:G433433  
A;Accession: S39526  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 133-513, 'A', '515-710, 'P', '712-730 <MA2>  
A;Cross-references: EMBL:X72795; NID:G433434; PIDN:CAA51315.1; PID:G433435  
R;Reponen, P.; Sahiberg, C.; Munaut, C.; Thesleff, I.; Tryggvason, K.  
J. Cell Biol. 124, 1091-1102, 1994  
A;Title: High expression of 92-kD type IV collagenase (gelatinase B) in the osteoclast  
A;Reference number: A54476; MUID:94179406; PMID:8132709  
A;Accession: I48296  
A;Molecule type: mRNA  
A;Residues: 1-513, 'A', '515-710, 'P', '712-730 <RES>  
A;Cross-references: EMBL:Z27231; NID:G415980; PIDN:CAA81745.1; PID:G415981  
C;Genetics:  
A;Gene: CLG4B  
A;Introns: 47/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 555/2; 602/2; 652/2; 6  
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol  
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-730/Product: progelatinase A #status predicted <PRO>  
F;108-730/Product: activation peptide #status predicted <ACT>  
F;213-388/Region: collagen binding #status predicted <MAT>  
F;230-271/Domain: fibronectin type II repeat homology <2F1>  
F;288-329/Domain: fibronectin type II repeat homology <2F2>  
F;347-388/Domain: fibronectin type II repeat homology <2F3>  
F;453-549/Region: PEST sequence  
F;529-729/Domain: hemopexin repeat homology <PXN>  
F;100-401, 405, 411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F;401, 405, 411/Binding site: zinc, catalytic (His) (active) #status predicted  
F;402/Active site: Glu #status predicted  
F;534-729/Disulfide bonds: #status predicted  
Query Match 82.8%; Score 213.5; DB 2; Length 730;  
Best Local Similarity 85.1%; Pred. No. 1.8e-20;  
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
QY 1 LQQLSLPTGELDSATLKAMTPRCGVDPDLGRFOTTEGLKWHHN 47  
DB 75 LQQLSLPTGELDSATLKAITPRCGVDPDVGRFQTFKG-LKWDHNN 120  
RESULT 8  
KCHU1  
stromelysin 1 (EC 3.4.24.17) precursor [validated] - human  
N;Alternate names: angiotensin-converting enzyme; collagenase activating protein; matrix  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1992 #sequence revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: A28156; C29157; A28399; A60964; S15427  
R;Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.  
J. Biol. Chem. 263, 6742-6745, 1988  
A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi  
A;Reference number: A28156; MUID:88198243; PMID:3360803  
A;Accession: A28156  
A;Molecule type: mRNA  
A;Residues: 1-44, 'E', '46-477 <SAU>  
A;Cross-references: UNIPROT:P08254; GB:J03209; NID:G188618; PIDN:AAA36321.1; PID:G188619  
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,  
Biochem. J. 240, 913-916, 1986  
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysi  
A;Reference number: A90336; MUID:87156645; PMID:3030290  
A;Accession: C29157  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-477 <WHI>  
A;Cross-references: EMBL:X05232; NID:G36632; PIDN:CAA28859.1; PID:G36633  
R;Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisele, A.Z.; Marmer, B.L.; Grant, G.A.;  
Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987  
A;Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specific  
A;Reference number: A28399; MUID:88016164; PMID:3477804  
A;Accession: A28399  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-49, 'G', '51-419, 'L', '421-477 <WIL>  
A;Cross-references: GB:U78045; NID:G1688257; PIDN:AAB36942.1; PID:G1688259  
A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by  
R;Lark, M.W.; Walakovic, L.A.; Shah, T.K.; Vanmiddlesworth, J.; Cameron, P.M.; Lin, T.Y.  
Connect. Tissue Res. 25, 49-65, 1990  
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta  
A;Reference number: A60964; MUID:91059606; PMID:2173990  
A;Accession: A60964  
A;Molecule type: protein  
A;Residues: 18-29; 100-108 <LAR>  
R;Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.  
Biochem. J. 276, 217-221, 1991  
A;Title: Purification of recombinant human prostromelysin. Studies on heat activation to  
A;Reference number: S15427; MUID:91248150; PMID:2039471  
A;Accession: S15427  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 18-23 <BIO>  
R;Lijnen, H.R.; Ugwa, F.; Bini, A.; Collen, D.  
Biochemistry 37, 4699-4702, 1998  
A;Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M  
A;Reference number: A58812; MUID:9548733; PMID:9548733  
A;Contents: annotation  
R;Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, February 1997  
A;Reference number: A68466; PDB:1HFS  
A;Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160  
R;Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.  
Protein Sci. 4, 1966-1976, 1995  
A;Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain an  
A;Reference number: A58914; MUID:96117647; PMID:8535233  
A;Contents: annotation; X-ray crystallography, 1.70 angstroms  
R;Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.  
Biochemistry 30, 6476-6483, 1991  
A;Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch  
A;Reference number: A39589; MUID:91274298; PMID:1647201  
A;Contents: annotation  
R;Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, August 1995  
A;Reference number: A66337; PDB:1SLM  
A;Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47; 57-267  
R;Gooley, P.R.; O'Connell, J.F.  
submitted to the Brookhaven Protein Data Bank, March 1995  
A;Reference number: A67284; PDB:2SRT  
A;Contents: annotation; conformation by (1)H-NMR, residues 100-272  
R;Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Ess  
Biochemistry 32, 13098-14008, 1993  
A;Title: Secondary structure and zinc ligation of human recombinant short-form stromelys  
A;Reference number: A58915; MUID:94059987; PMID:8241164  
A;Contents: annotation; conformation by (1)H-NMR  
C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation  
C;Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of whi  
C;Genetics:  
A;Gene: GDB:MMP3; STMY; STMY1  
A;Cross-references: GDB:I120727; OMIM:185250  
A;Map position: 11q23-11q23  
C;Function:  
A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si  
A;Note: degrades various extracellular matrix proteins, including fibronectin, plasminog  
plasminogen to yield a fragment with angiostatin activity  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKW 43

Query Match 51.9%; Score 134; DB 1; Length 475;  
Best Local Similarity 53.2%; Pred. No. 5.4e-10;  
Matches 25; Conservative 7; Mismatches 15; Indels

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47

Db 65 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRWKH 111

RESULT 11

JC6505

stromelysin 2 (EC 3.4.24.22) precursor - mouse

N:Alternate names: matrix metalloproteinase 10

C:Species: Mus musculus (house mouse)

C>Date: 16-Oct-1998 #sequence\_revision 16-Oct-1998 #text\_change 09-Jul-2004

C:Accession: J06505

R:Madlener, M.; Werner, S.

Gene 202, 75-81, 1997

A:Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).

A:Reference number: JC6505; MUID:98087420; PMID:9427548

A:Accession: J06505

A:Molecule type: mRNA

A:Residues: 1-476 <WAD>

A:Cross-references: UNIPROT:O55123; GB:Y13185; NID:G2791311; PIDN:CRA73641.1; PID:G27913

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C:Genetics:

A:Gene: MMP-10

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-476/Product: prostromelysin 2 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:91-217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:119/Binding site: carboxylate (Asn) (covalent) #status predicted

F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted

F:218/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Cy 1 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKW 43

Db 67 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRWKH 109

RESULT 12

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor [validated] - human

N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: A28816; A47496

R:Miller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988

A:Title: The collagenase gene family in humans consists of at least four members.

A:Reference number: A90339; MUID:88339885; PMID:2844164

A:Accession: A28816

A:Molecule type: mRNA

A:Residues: 1-476 <WUL>

A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36628

A:Note: mRNA for this protein was detected in several human tumors

R:Windor, L.J.; Grenett, R.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993

A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene

A:Reference number: A47496; MUID:93352520; PMID:8349617

A:Accession: A47496

A:Molecule type: protein

A:Residues: 17-33 <WIN>

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin

C:Genetics:

A:Gene: GDB:MMP10; STWY2

A:Cross-references: GDB:120392; OMIM:185260

A:Map position: 11q22.3-11q23

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-476/Product: prostromelysin 2 #status experimental <PRO>

F:17-98/Domain: activation peptide #status predicted <ACT>

F:59-263/Domain: matrix metalloproteinase homology <MMP>

F:89-96/Region: autoinhibitory

F:99-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:91-217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:119/Binding site: carboxylate (Asn) (covalent) #status predicted

F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted

F:218/Active site: Glu #status predicted

F:289-476/Disulfide bonds: #status predicted

Query Match 51.6%; Score 133; DB 1; Length 476;

Best Local Similarity 58.1%; Pred. No. 7.4e-10;

Matches 25; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Cy 1 LOKQLSLPETGELDSATLKAMRTPRCGVPDLGRFOTFEGDLKW 43

Db 66 MQKFLGLKMTGKLDNTMLMKPCGVPDVGGFSTFGSPKRWKH 108

RESULT 13

KCHUS2

stromelysin 2 (EC 3.4.24.22) precursor - rat

N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: B26403; A41775; S26498

R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P. Nucleic Acids Res. 15, 1139-1151, 1987

A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a

A:Reference number: A26403; MUID:87146421; PMID:3547333

A:Accession: B26403

A:Molecule type: mRNA

A:Residues: 1-476 <BRE>

A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57388

A:Note: intron positions were determined by comparison of the cDNA sequence to genomic s

P:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Es J. Biol. Chem. 267, 1099-1103, 1992

A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ

A:Reference number: A41775; MUID:92112748; PMID:1370458

A:Accession: A41775

A:Molecule type: mRNA

A:Residues: 1-476 <CHA>

A:Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151

A:Note: sequence extracted from NCBI backbone (NCBI:76184)

R:de Vries, M.W.; Mukherjee, B.B. Oncogene 7, 109-119, 1992

A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra

A:Reference number: S26496; MUID:92158347; PMID:1741158

A:Accession: S26498

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 31-103, 'L', 241-242, 'TQMEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>

A:Cross-references: EMBL:X64020

C:Genetics:

A:Introns: 35/3; 117/1; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-476/Product: prostromelysin 2 #status predicted <PRO>

F:18-99/Domain: activation peptide #status predicted <ACT>

F:60-264/Domain: matrix metalloproteinase homology <MMP>

F:90-97/Region: autoinhibitory

F:100-476/Product: stromelysin 2 #status predicted <MAT>

F:283-476/Domain: hemopexin repeat homology <PXN>

F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F:120/Binding site: carboxylate (Asn) (covalent) #status predicted

F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 96.4103 Seconds  
(without alignments)  
280.495 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQKQLSLPTGELDSATLKA.....VPLDLRFQTFEGDLKWHHN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	707	1 MM09_HUMAN	P14780 homo sapien
2	235	91.1	707	1 MM05_RABIT	P41246 oryctolagus
3	233	90.3	708	1 MM05_RAT	P50282 rattus norv
4	226	87.6	324	2 Q9N282	Q9N282 bos taurus
5	226	87.6	712	1 MM09_BOVIN	P52176 bos taurus
6	216	83.7	149	2 Q9TVB4	Q9TVB4 canis famil
7	216	83.7	704	1 MM09_CANFA	O18733 canis famil
8	216	83.7	704	2 O19130	O19130 canis famil
9	216	83.7	704	2 Q71U09	Q71U09 canis famil
10	216	83.7	704	2 AAD50275	AAD50275 canis fam
11	213.5	82.8	730	1 MM05_MOUSE	P41245 mus musculu
12	213.5	82.8	730	2 Q80X18	Q80X18 mus musculu
13	193	74.8	679	2 Q98856	Q98856 cynops pyrr
14	185	71.7	686	2 Q9DE15	Q9DE15 gallus gall
15	177	68.6	673	2 Q90YB3	Q90YB3 paralicichy
16	176	68.2	671	2 Q6PF33	Q6PF33 xenopus lae
17	176	68.2	671	2 Q9W7L6	Q9W7L6 xenopus lae
18	176	68.2	671	2 AAH57745	AAH57745 xenopus l
19	172	66.7	675	2 Q8QFQ6	Q8QFQ6 oncorhynch
20	170	65.9	674	2 Q98TC6	Q98TC6 cyprinus ca
21	168	65.1	690	2 Q9PYM5	Q9PYM5 oryzias lat
22	167	64.7	670	2 Q6DF16	Q6DF16 xenopus tro
23	160	62.0	680	2 Q7T317	Q7T317 brachydanio
24	141	54.7	477	1 MM03_HUMAN	P08254 homo sapien
25	141	54.7	477	2 AAH53676	AAH53676 homo sapi
26	141	54.7	477	2 AAH59716	AAH59716 homo sapi
27	138	53.5	478	1 MM03_RABIT	P28863 oryctolagus
28	135	52.3	145	2 Q9N283	Q9N283 bos taurus
29	134	51.9	475	1 MM03_RAT	P03957 rattus norv
30	133	51.6	139	2 Q9GM68	Q9GM68 sus scrofa
31	133	51.6	476	1 MM10_HUMAN	P09238 homo sapien

## RESULT 1

ID	MM09_HUMAN	STANDARD;	PRT;	707 AA.
AC	P14780; Q8N725; Q9H421;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa			
DE	gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)			
DE	(GELS)			
GN	Name=MMP9; Synonyms=CLG4B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.			
RP	MEDLINE=90008879; PubMed=22551898;			
RA	Wilhelm S.M., Collier I.E., Marmer B.L., Eisen A.Z., Grant G.A.,			
RA	Goldberg G.I.;			
RT	"SV40-transformed human lung fibroblasts secrete a 92-kDa type IV			
RT	collagenase which is identical to that secreted by normal human			
RT	macrophages.";			
RL	J. Biol. Chem. 264:17213-17221(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91358433; PubMed=1653238;			
RA	Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J.,			
RA	Tryggvason K.;			
RT	"Complete structure of the human gene for 92-kDa type IV collagenase.			
RT	Divergent regulation of expression for the 92- and 72-kilodalton			
RT	enzyme genes in Ht-1080 cells.";			
RL	J. Biol. Chem. 266:16485-16490(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT GUN-279.			
RP	Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,			
RA	Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;			
RA	"SeattlesNP. NLEBI HL66682 program for genomic applications, UN-			
RT	PHCC, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (AUG-2002) to the ENEL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT GUN-279.			
RP	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			

## ALIGNMENTS

32	133	51.6	476	1	MM10_MOUSE
33	133	51.6	476	1	MM10_RAT
34	133	51.6	476	2	AA335110
35	133	51.6	477	1	MM03_MOUSE
36	133	51.6	479	2	Q922W6
37	131	50.8	478	2	Q6Y4Q5
38	131	50.8	478	2	AA063580
39	128	49.6	167	2	Q7ZWD0
40	128	49.6	465	1	MM08_MOUSE
41	128	49.6	465	2	Q8C209
42	128	49.6	465	2	Q8C230
43	128	49.6	465	2	AA442742
44	128	49.6	465	2	BAC40805
45	128	49.6	466	1	MM08_RAT

O55123 mus musculu  
P07152 rattus norv  
Aap36110 homo sapi  
P28862 mus musculu  
Q922w6 mus musculu  
Q6y4q5 canis famil  
AA063580 canis fam  
Q7zwd0 brachydanio  
Q70138 mus musculu  
Q8C209 mus musculu  
Q8C230 mus musculu  
AA442742 mus muscu  
BAC40805 mus muscu  
O88765 rattus norv

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.D., McConachie L.J., Mclay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sethra H.K., Showkeen R., Sims S.,  
RA Suke C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Syamcore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.,  
RT "The DNA sequence and comparative analysis of human chromosome 20";  
RL Nature 414:865-871(2001).  
[5]  
RN SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Schenck C.M., Schuler G.D.,  
RA Altschul S.F., Zerbberg B., Buetkow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.J., Skalska U.,  
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RN SEQUENCE OF 1-11 FROM N.A.  
RX MEDLINE=93149601; PubMed=8426746;  
RA Sato H., Seiki M.,  
RT "Regulatory mechanism of 92 kDa type IV collagenase gene expression  
which is associated with invasiveness of tumor cells";  
RL Oncogene 8:395-405(1993).  
[7]  
RN SEQUENCE OF 20-37.  
RX MEDLINE=91355647; PubMed=1653055;  
RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,  
RA Auerx J., van Damme J., Opdenakker G.,  
RT "The cytokine-protease connection: identification of a 96-kD THP-1  
gelatinase and regulation by interleukin-1 and cytokine inducers";  
RL Cytokine 3:231-239(1991).  
[8]  
RN SEQUENCE OF 28-60.  
RX TISSUE=Neutrophils;  
RA Masure S., Proost P., van Damme J., Opdenakker G.,  
RA "Purification and identification of 91-kDa neutrophil gelatinase.  
Release by the activating peptide dermoneurin-8";  
RL Eur. J. Biochem. 198:391-398(1991).  
[9]  
RN CHARACTERIZATION.  
RA Kang K., Lee D.-H.,  
RT "Purification and characterization of human 92-kDa type IV collagenase  
(gelatinase B)";  
RL Exp. Mol. Med. 28:161-165(1996).  
[10]  
RN 3D-STRUCTURE MODELING.  
RA Mallena S.C., Sagarikar R.D.,  
RT "Theoretical model of human type IV collagenase precursor";

RL Submitted (APR-2002) to the PDB data bank.  
[11]  
RN VARIANTS VAL-20; LYS-82 AND GLN-279.  
RX MEDLINE=20065865; PubMed=10598806;  
RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.,  
RT "Genetic variation at the matrix metalloproteinase-9 locus on  
chromosome 20q12.2-13.1";  
RL Hum. Genet. 105:418-423(1999).  
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.  
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen  
types IV and V.  
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
CC -!- SUBUNIT: Exists as monomer, disulfide-linked homodimer, and as a  
heterodimer with a 25 kDa protein. Macrophages and transformed  
cell lines produce only the monomeric form.  
CC -!- TISSUE SPECIFICITY: Produced by normal alveolar macrophages and  
granulocytes.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 3 fibronectin type II domains.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
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CC -----  
CC EMBL: J05070; AA51539.1; -  
CC EMBL: D10051; BAA20967.1; -  
CC EMBL: AF538844; AAM97934.1; -  
CC EMBL: AL162458; CAC10459.1; -  
CC EMBL: BC060693; AAH06093.1; -  
CC FIC: A34458; A34458.  
CC PDB: 1GKC; X-ray; A/B=106-443.  
CC PDB: 1GKD; X-ray; A/B=106-443.  
CC PDB: 1LTV; X-ray; A/B=513-707.  
CC PDB: 1L6J; X-ray; A=20-444.  
CC PDB: 1LKG; Model; A=1-707.  
CC MEROPS: M10.004; -  
CC GlycoSuiteDB: P14780; -  
CC Genew: HGNC:7176; MMP9.  
CC MTM: 120361; -  
CC GO: GO:0005615; C:extracellular space; TAS.  
CC GO: GO:0008133; F:collagenase activity; TAS.  
CC GO: GO:0008270; F:zinc ion binding; TAS.  
CC GO: GO:0006508; P:proteolysis and peptidolysis; TAS.  
CC InterPro: IPR000562; FN Type II.  
CC InterPro: IPR000585; Hemopexin.  
CC InterPro: IPR001818; Pept\_M10A\_M12B.  
CC InterPro: IPR006025; Pept\_M\_Zn\_BS.  
CC InterPro: IPR009070; PGD\_Like.  
CC InterPro: IPR006970; PT.  
CC Pfam: PF00040; fn2; 3.  
CC Pfam: PF00045; Hemopexin; 4.  
CC Pfam: PF00413; Peptidase M10; 1.  
CC Pfam: PF03933; Peptidase M10\_N; 1.  
CC Pfam: PF04886; PT; 1.  
CC PRINTS: PR00013; FNTYPEII.  
CC PRINTS: PR00138; MATRXIN.  
CC ProDom: PD000995; FN\_Type\_II; 3.  
CC PROSITE: PS00546; CYSTEINE\_SWITCH; 1.  
CC PROSITE: PS00023; FIBRONECTIN\_2; 3.  
CC PROSITE: PS00024; HEMOPEXIN; 1.  
CC PROSITE: PS00142; ZINC\_PROTEASE; 1.  
CC 3D-structure; Calcium; Collagen degradation;  
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;  
KW Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;  
KW Zymogen.  
FT SIGNAL 1 19  
FT PROPEP 20 106  
FT CHAIN 107 707  
FT Activation peptide.  
FT 92 kDa type IV collagenase.

```

FT DOMAIN 223 280 Fibronection type-II 1.
FT DOMAIN 281 339 Fibronection type-II 2.

Query Match 100.0%; Score 258; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGLKWHHN 47
Db 74 LQKLSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGLKWHHN 120

RESULT 2
MM09 RABBIT
ID MM09 RABBIT STANDARD; PRT; 707 AA.
AC P41246;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=MMP9;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese White; TISSUE=Bone;
RX MEDLINE=94253056; PubMed=8195136;
RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts.";
RL J. Biol. Chem. 269:15006-15009(1994).
RN [2]
RP SEQUENCE OF 1-171 FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=95050662; PubMed=7961810;
RA Fini M.E., Bartlett J.D., Matsubara M., Rinehart W.B., Mody M.K.,
RA Girard M.T., Rainville M.;
RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and
RT AP2 in cell type-specific transcription.";
RL J. Biol. Chem. 269:28620-28628(1994).
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -!- TISSUE SPECIFICITY: Osteoclasts.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 3 fibronection type II domains.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
CC EMBL; D26514; BAA03520.1; -
CC EMBL; L36050; AAA64358.1; -
CC PIR; A53796; A53796.
CC HSSP; P14780; 1GKC.
CC -----
CC MEROPS; M10.004; -.
CC InterPro; IPR000562; FN Type_II.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR018181; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR009070; PGSD_like.
CC InterPro; IPR006970; PT.

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DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04896; PT; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRXIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 19 By similarity.
FT PROPEP 20 106 Activation peptide (By similarity).
FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronection type-II 1.
FT DOMAIN 281 339 Fibronection type-II 2.
FT DOMAIN 340 397 Fibronection type-II 3.
FT DOMAIN 513 707 Hemopexin-like.
FT SITE 99 99 Cysteine switch (By similarity).
FT METAL 401 401 Zinc (catalytic) (By similarity).
FT ACT_SITE 402 402 By similarity.
FT METAL 405 405 Zinc (catalytic) (By similarity).
FT METAL 411 411 Zinc (catalytic) (By similarity).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT DISULFID 516 704 By similarity.
FT CONFLICT 76 76 K->P (in Ref. 2).
FT CONFLICT 100 102 GVP->ASR (in Ref. 2).
SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 4.1e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGLKWHHN 47
Db 74 LQKLSLPETGELDSATLKAMETPRCGVDPDLGRFOTFEGLKWHHN 120

RESULT 3
MM09 RAT
ID MM09 RAT STANDARD; PRT; 708 AA.
AC P50282;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=96184505; PubMed=8605986;
RA Xia Y., Garcia G., Chen S., Wilson C.B., Feng L.;
RT "Cloning of rat 92-kDa type IV collagenase and expression of an active
RT recombinant catalytic domain.";
RL FEBS Lett. 382:285-288(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=96069602; PubMed=7590350;

```

RA Okada A., Santavica M., Bassett P.;  
 RT "The cDNA cloning and expression of the gene encoding rat gelatinase  
 B.";  
 RL Gene 164:317-321(1995).  
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.  
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen  
 CC types IV and V.  
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; U36476; AA01721.1; -;  
 DR EMBL; U24441; AA90911.1; -;  
 DR PIR; JC4364; JC4364.  
 DR PIR; S62907; S62907.  
 DR HSSP; P14780; IGKC.  
 DR MEROPS; M10.004; -;  
 DR RGD; 621320; Mmp9; -;  
 DR InterPro; IPR000562; FN\_Type\_II.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR006970; PT.  
 DR Pfam; PF00040; fn2; 3.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR Pfam; PF04886; PT; 1.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00138; MATRXIN.  
 DR ProDom; PD000995; FN\_Type\_II; 3.  
 DR SMART; SM00059; FN2; 3.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZmMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
 KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 19  
 FT PROPEP 20 107  
 FT CHAIN 108 708  
 FT DOMAIN 224 281  
 FT DOMAIN 282 340  
 FT DOMAIN 341 398  
 FT DOMAIN 516 708  
 FT SITE 100 100  
 FT METAL 402 402  
 FT ACT\_SITE 403 403  
 FT METAL 406 406  
 FT METAL 412 412  
 FT CARBOHYD 39 39  
 FT CARBOHYD 121 121  
 FT DISULFID 519 707  
 FT CONFLICT 2 2  
 FT CONFLICT 112 112  
 FT CONFLICT 326 327  
 FT CONFLICT 364 364  
 FT CONFLICT 441 441  
 FT CONFLICT 472 472  
 FT CONFLICT 515 515  
 FT CONFLICT 551 551

FT CONFLICT 566 566 F -> L (in Ref. 2).  
 FT CONFLICT 568 568 S -> A (in Ref. 2).  
 FT CONFLICT 579 579 P -> S (in Ref. 2).  
 FT CONFLICT 586 589 LWAQ -> SGRK (in Ref. 2).  
 FT CONFLICT 597 597 S -> T (in Ref. 2).  
 FT CONFLICT 669 669 Q -> H (in Ref. 2).  
 SQ SEQUENCE 708 AA; 78610 MW; D57DCOD1B93A778C CRC64;  
 Query Match 90.3%; Score 233; DB 1; Length 708;  
 Best Local Similarity 85.1%; Pred. No. 7.6e-23;  
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 QY 1 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47  
 DB 75 LQKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 121  
 RESULT 4  
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 ID QN282  
 AC QN282;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MWP-9 (Fragment).  
 GN Name=bmp-9;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sato T., Hirata M., Ito A., Hashizume K.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB043996; BAA96389.1; -;  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000562; Peptidase M.  
 DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR Pfam; PF00040; fn2; 3.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00138; MATRXIN.  
 DR ProDom; PD000995; FN\_Type\_II; 3.  
 DR SMART; SM00059; FN2; 3.  
 DR SMART; SM00235; ZmMc; 1.  
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 DR PROSITE; PS00023; FIBRONECTIN\_2; 1.  
 DR NON\_TER 324 324  
 SQ SEQUENCE 324 AA; 36273 MW; 4137C9820C28E080 CRC64;  
 Query Match 87.6%; Score 226; DB 2; Length 324;  
 Best Local Similarity 84.8%; Pred. No. 2.8e-22;  
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 QKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47  
 DB 75 QKQLSLPETGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 120  
 RESULT 5  
 MM09\_BOVIN STANDARD; PRT; 712 AA.  
 ID MM09\_BOVIN  
 AC P52176;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa  
 DE Gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)

DE (GELB).  
GN Name=MMP9;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]\_SEQUENCE FROM N.A.  
RP TISSUE=Leukocyte;  
RC MEDLINE=95287902; PubMed=7770085;  
RX Baylis H.A., Megson A., Hall R.;  
RA "Infection with Theileria annulata induces expression of matrix  
RT metalloproteinase 9 and transcription factor Ap-1 in bovine  
RT leucocytes";  
RL Mol. Biochem. Parasitol. 69:211-222(1995).  
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.  
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen  
CC types IV and V.  
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 3 fibronectin type II domains.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC  
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CC or send an email to [licens@isb-sib.ch](mailto:licens@isb-sib.ch)).  
CC  
CC -----  
CC EMBL; X78324; CAA55127.1; -.  
CC PIR; I46031; I46031.  
CC HSP; P14780; IGKD.  
CC  
CC MEROPS: M10.004; -.  
CC InterPro; IPR000562; FN\_Type\_II.  
CC InterPro; IPR000585; Hemopexin.  
CC InterPro; IPR006026; Peptidase M.  
CC InterPro; IPR001818; Pept\_M10A\_M12B.  
CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
CC InterPro; IPR009070; PGBD\_like.  
CC InterPro; IPR006970; PT.  
CC Pfam; PF00040; fn2; 3.  
CC Pfam; PF00045; Hemopexin; 4.  
CC Pfam; PF00413; Peptidase M10; 1.  
CC Pfam; PF03933; Peptidase\_M10\_N; 1.  
CC Pfam; PF04886; PT; 1.  
CC PRINTS; PR00013; FNTYPEII.  
CC PRINTS; PR00138; MATRXIN.  
CC ProDom; PD00095; FN\_Type\_II; 3.  
CC SMART; SM00059; FN2; 3.  
CC SMART; SM00120; HX; 4.  
CC SMART; SM00235; ZtMC; 1.  
CC PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
CC PROSITE; PS00023; FIBRONECTIN\_2; 3.  
CC PROSITE; PS00024; HEMOPEXIN\_FALSE\_NEG.  
CC PROSITE; PS00142; ZINC\_PROTEASES; 1.  
CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
CC Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.  
CC SIGNAL 1 19  
CC By similarity.  
CC PROPEP 20 106 Activation peptide.  
CC CHAIN 107 712 92 kDa type IV collagenase.  
CC DOMAIN 223 280 Fibronectin type-II 1.  
CC DOMAIN 281 339 Fibronectin type-II 1.  
CC DOMAIN 340 397 Fibronectin type-II 3.  
CC DOMAIN 518 712 Hemopexin-like.  
CC SITE 99 99 Cysteine switch (By similarity).  
CC METAL 401 401 Zinc (catalytic) (By similarity).  
CC ACT\_SITE 402 402 Zinc (catalytic) (By similarity).  
CC METAL 405 405 Zinc (catalytic) (By similarity).  
CC METAL 411 411 Zinc (catalytic) (By similarity).  
CC DISULFID 521 709 By similarity.

FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 712 AA; 79087 MW; E7FDA28372AE30CE CRC64;  
Query Match 87.6%; Score 226; DB 1; Length 712;  
Best Local Similarity 84.8%; Pred. No. 7e-22; Indels 0; Gaps 0;  
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 QKQSLPFGELSDATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47  
Db 75 QRRLSLPETGELSDTTLNAPRCGVDPVGRVQTFEGELKWHHN 120  
  
RESULT 6  
Q9TVB4 PRELIMINARY; PRT; 149 AA.  
ID Q9TVB4  
AC Q9TVB4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Type IV collagenase MMP-9 (Fragment).  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibrosarcoma;  
RA Paria B.C., Kitchell B.E.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF147104; AAD31323.1; -.  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR009070; PGBD\_like.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00138; MATRXIN.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
CC Collagen.  
FT NON\_TER 149 149  
SQ SEQUENCE 149 AA; 17025 MW; CA6A5062EFD0CBFF CRC64;  
Query Match 83.7%; Score 216; DB 2; Length 149;  
Best Local Similarity 78.7%; Pred. No. 2.7e-21;  
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
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Db 74 LQRLALPETGELDKTTLEAMRAPRCGVDPDLGRFQTFEGDLKWHND 120  
  
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MM09 CANFA STANDARD; PRT; 704 AA.  
ID MM09 CANFA  
AC O18733;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa  
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)  
DE (GELB).  
GN Name=MMP9;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mongrel;  
RX MEDLINE=21587576; PubMed=11731079; DOI=10.1016/S0304-4165(01)00192-1;

RA Yokota H., Kumata T., Takekaba S., Kobayashi T., Moue H., Taniyama H.,  
RA Hirayama K., Kagawa Y., Itoh N., Fujita O., Nakade T., Yuasa A.,  
RT "High expression of 92 kDa type IV collagenase (matrix  
RT Metalloproteinase-9) in canine mammary adenocarcinoma.";  
RL Biochim. Biophys. Acta 1569:7-12(2001).  
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.  
CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen  
CC types IV and V.  
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 3 fibronectin type II domains.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC -----  
CC EMBL; AB06421; BAA22087.3; --  
CC HSSP; P14780; IGKC.  
CC MEROPS; M10.004; --  
CC InterPro; IPR000562; FN\_Type\_II.  
CC InterPro; IPR000585; Hemopexin.  
CC InterPro; IPR006026; Peptidase M.  
CC InterPro; IPR001818; Pept\_M10A\_M12B.  
CC InterPro; IPR006025; Pept\_M\_Zn\_BS.  
CC InterPro; IPR009070; PGSD\_like.  
CC InterPro; IPR006970; PT.  
CC Pfam; PF00040; fn2; 3.  
CC Pfam; PF00045; Hemopexin; 4.  
CC Pfam; PF00413; Peptidase M10; 1.  
CC Pfam; PF03933; Peptidase\_M10\_N; 1.  
CC Pfam; PF04886; PT; 1.  
CC PRINTS; PR00013; FNTYPEII.  
CC PRINTS; PR00138; MATRXIN.  
CC ProDom; PD000995; FN\_Type\_II; 3.  
CC SMART; SM00059; FN2; 3.  
CC SMART; SM00120; HX; 4.  
CC SMART; SM00235; ZMC; 1.  
CC PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
CC PROSITE; PS00023; FIBRONECTIN\_2; 3.  
CC PROSITE; PS00024; HEMOPEXIN; FALSE NEG.  
CC PROSITE; PS00142; ZINC\_PROTEASE; 1.  
CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;  
KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.  
FT SIGNAL 1 19  
FT PROPEP 20 106 Activation peptide (By similarity).  
FT CHAIN 107 704 92 kDa type IV collagenase.  
FT DOMAIN 223 280 Fibronectin type-II 1.  
FT DOMAIN 281 339 Fibronectin type-II 2.  
FT DOMAIN 340 397 Fibronectin type-II 3.  
FT DOMAIN 445 508 Pro-rich.  
FT DOMAIN 510 704 Hemopexin-like.  
FT METAL 401 401 Zinc (catalytic) (By similarity).  
FT ACT\_SITE 402 402 By similarity.  
FT METAL 405 405 Zinc (catalytic) (By similarity).  
FT METAL 411 411 Zinc (catalytic) (By similarity).  
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).  
FT DISULFID 127 127 N-linked (GlcNAc...) (Potential).  
FT SIGNAL 513 701 By similarity.  
SQ SEQUENCE 704 AA; 81123 MW; 0D3394D26256B91 CRC64;  
Query Match 83.7%; Score 216; DB 1; Length 704;  
Best Local Similarity 78.7%; Pred. No. 1.6e-20;  
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LQKQLSLPETGELDSATLKAVETPCGVPDLGRFQTFEGDLKWHHN 47  
DB 74 LQRLALPETGELDKTTLLEAPRCGVPDLGKGFQTFEGDLKWHND 120

RESULT 8  
O19130 PRELIMINARY; PRT; 704 AA.  
ID O19130;  
AC O19130;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Gelatinase B.  
DE Canis familiaris (Dog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97467354; PubMed=9325284;  
RA Fang K.C., Raymond W.W., Blount J.L., Caughey G.H.;  
RT "Dog mast cell alpha-chymase activates progelatinase B by cleaving the  
RT Phe88-Gln89 and Phe91-Glu92 bonds of the catalytic domain.";  
RL J. Biol. Chem. 272:25628-25635(1997).  
DR EMBL; U9842; AAB81681.1; --  
DR HSSP; P14780; IGKC.  
DR GO; GO:0003578; C:extracellular matrix; IEA.  
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000562; FN\_Type\_II.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR009070; PGSD\_like.  
DR InterPro; IPR006970; PT.  
DR Pfam; PF00040; fn2; 3.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR Pfam; PF04886; PT; 1.  
DR PRINTS; PR00013; FNTYPEII.  
DR PRINTS; PR00138; MATRXIN.  
DR ProDom; PD000995; FN\_Type\_II; 2.  
DR SMART; SM00059; FN2; 3.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00023; FIBRONECTIN\_2; 3.  
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
DR SEQUENCE 704 AA; 78259 MW; AF9999247E463318 CRC64;  
Query Match 83.7%; Score 216; DB 2; Length 704;  
Best Local Similarity 78.7%; Pred. No. 1.6e-20;  
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LQKQLSLPETGELDSATLKAVETPCGVPDLGRFQTFEGDLKWHHN 47  
DB 74 LQRLALPETGELDKTTLLEAPRCGVPDLGKGFQTFEGDLKWHND 120

RESULT 9  
Q71U09 PRELIMINARY; PRT; 704 AA.  
ID Q71U09;  
AC Q71U09;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Matrix metalloproteinase-9.  
DE Canis familiaris (Dog).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibrosarcoma;



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RA Paria B.C., Balkin R.G., Kitchell B.E.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169244; AAD50275.1; -
DR InterPro; IPR000562; FN_Type II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006036; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; FGBD_like.
DR InterPro; IPR006970; PT.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04896; PT_1.
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DR PRINTS; PD00138; MATRIXIN.
DR ProDom; PD000995; FN_Type II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 704 AA; 78198 MW; A3935A2C8F85CDD7 CRC64;

Query Match 83.7%; Score 216; DB 2; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47
Db LQRLALPTGELDKTTLKAMRACPGVDPDLGRFOTFEGDLKWHND 120

RESULT 10
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AC AAD50275;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase-9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibrosarcoma;
RA Paria B.C., Balkin R.G., Kitchell B.E.;
RT "Partial cloning of canine type-IV (MMP-9) from canine fibrosarcoma.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF169244; AAD50275.1; -
SQ SEQUENCE 704 AA; 78198 MW; A3935A2C8F85CDD7 CRC64;

Query Match 83.7%; Score 216; DB 2; Length 704;
Best Local Similarity 78.7%; Pred. No. 1.6e-20;
Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQKQLSLPTGELDSATLKAMRTPCGVDPDLGRFOTFEGDLKWHHN 47
Db LQRLALPTGELDKTTLKAMRACPGVDPDLGRFOTFEGDLKWHND 120

RESULT 11
MM09_MOUSE STANDARD; PRT; 730 AA.
ID MM09_MOUSE
AC P41345; Q06788; Q9DC02;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

```

DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9; Synonyms=C1g4b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RA MEDLINE=94179406; PubMed=8132709;
RX Reponen P., Sahlberg C., Munaut C., Thesleff I., Tryggvason K.;
RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
RT osteoclast lineage during mouse development.";
RL J. Cell Biol. 124:1091-1102(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=93176173; PubMed=8382489;
RX Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 190:732-740(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=94062823; PubMed=8243459;
RA Masure S., Nys G., Fiten P., van Damme J., Odenakker G.;
RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
RT glycosylation in WH1-3 macrophages and gene organisation.";
RL Eur. J. Biochem. 218:129-141(1993).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE=9403534; PubMed=8219207;
RX Graubert T., Johnston J., Berliner N.;
RT "Cloning and expression of the cDNA encoding mouse neutrophil
RT gelatinase: demonstration of coordinate secondary granule protein gene
RT expression during terminal neutrophil maturation.";
RL Blood 82:3192-3197(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=9403534; PubMed=8219207;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Boro H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bract D., Brueic V., Clothia C., Corbani L.B., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Binney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.

```



QY	1	LOKQLSLPETGELDSATLKAMT	PRCGVPDLGRFQTTFEGDLKWHHN	47
Db	75	MQKQLGLNETGELDQSTLEAMKTPRCGVPDVGNGFQTFDGLKWDHND	121	
RESULT 14				
Q9DE15		PRELIMINARY;	PRT;	686 AA.
ID	Q9DE15			
AC	Q9DE15			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	75 kDa gelatinase.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20576236; PubMed=11010969;			
RA	Hahn-Dantona E.A., Aimes R.T., Quigley J.P.;			
RT	"The isolation, characterization, and molecular cloning of a 75-kDa			
RT	gelatinase B-like enzyme, a member of the matrix metalloproteinase			
RT	(MMP) family. An avian enzyme that is MMP-9-like in its cell			
RT	expression pattern but diverges from mammalian gelatinase B in			
RT	sequence and biochemical properties."			
RL	J. Biol. Chem. 275:40827-40838(2000).			
DR	EMBL; AF222690; AAG47650.1; --			
DR	HSSP; P33435; 1CXV.			
DR	MEROFS; M10.004; --			
DR	GO; GO:0005578; C:extracellular matrix; IEA.			
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000562; FN_Type_II.			
DR	InterPro; IPR000585; Hemopexin.			
DR	InterPro; IPR006026; Peptidase M.			
DR	InterPro; IPR001818; Pept_M10A_M12B.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR009070; PGED_like.			
DR	Pfam; PF00040; fn2; 3.			
DR	Pfam; PF00045; Hemopexin; 4.			
DR	Pfam; PF00413; Peptidase M10; 1.			
DR	Pfam; PF03933; Peptidase M10_N; 1.			
DR	PRINTS; PR00013; FNTPPEIT.			
DR	ProDom; PD000995; FN_Type_II; 2.			
DR	SMART; SM00059; FN2; 3.			
DR	SMART; SM00120; HX; 4.			
DR	SMART; SM00235; ZnMC; 1.			
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.			
DR	PROSITE; PS00023; FIBRONECTIN_2; 3.			
DR	PROSITE; PS00024; FIBRONECTIN_1.			
DR	PROSITE; PS00024; HEMOPEXIN; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.			
SQ	SEQUENCE 686 AA; 76679 MW; 9E9A59F96A497CE CRC64;			
Query Match 71.7%; Score 185; DB 2; Length 686;				
Best Local Similarity 73.3%; Pred. No. 2.8e-16;				
Matches 33; Conservative 6; Mismatches 6; Indels 0; Gaps 0;				
QY	1	LOKQLSLPETGELDSATLKAMT	PRCGVPDLGRFQTTFEGDLKWHH	45
Db	74	MQKQLGLSETGELDASTLEAMRPRCGVPDVGGLTFEGELKWDH	118	
RESULT 15				
Q90YB3		PRELIMINARY;	PRT;	673 AA.
ID	Q90YB3			
AC	Q90YB3			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Gelatinase.			



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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 102.462 Seconds  
(without alignments)  
189.060 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292  
Sequence: 1 MQEFFGLKVTGRDAETLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Geneseq 23Sep04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17092 Human mat
4	292	100.0	454	7	ADL16002 G-coupled
5	292	100.0	454	7	ADL16004 G-coupled
6	292	100.0	454	7	ADL16006 G-coupled
7	292	100.0	454	7	ADL16008 G-coupled
8	292	100.0	454	8	ADL19345 Human G-c
9	292	100.0	454	8	ADL19343 Human G-c
10	292	100.0	455	8	ADL19341 Human G-c
11	292	100.0	469	4	AB84606 Amino aci
12	292	100.0	469	4	ABE10415 Human mat
13	292	100.0	469	6	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU56596 Lung can
18	292	100.0	469	6	ABU56597 Lung can
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ABD79176 Matrix me
22	292	100.0	469	7	ABE34550 Human ski
23	292	100.0	469	7	ABE16000 G-coupled
24	292	100.0	469	7	ABE16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

26	292	100.0	469	7	ADN38694 Cancer/an
27	292	100.0	469	7	ADN38696 Cancer/an
28	292	100.0	469	7	ADN39850 Cancer/an
29	292	100.0	469	7	ADN95538 Human BEC
30	292	100.0	469	8	ADL93949 Human G-C
31	292	100.0	469	8	ADL93939 Human G-C
32	292	100.0	470	8	ADN07695 Human mat
33	292	100.0	490	7	ADN07892 Novel pro
34	292	100.0	496	4	AA975509 Human col
35	286	97.9	457	1	AA93628 Sequence
36	286	97.9	469	1	AA970611 Sequence
37	286	97.9	469	8	ADQ18359 Human sof
38	285	97.6	454	8	ADL93947 Human G-C
39	233	79.8	43	6	ABP97139 Human mat
40	233	79.8	43	6	ABG76325 Human mat
41	233	79.8	43	8	ADQ17100 Human mat
42	214	73.3	55	6	ABP97132 Human mat
43	214	73.3	55	6	ABG76318 Human mat
44	214	73.3	55	8	ADQ17093 Human mat
45	214	73.3	444	4	AA65357 Human MMP

ALIGNMENTS

RESULT 1

ABP97131  
ID ABP97131 standard; peptide; 54 AA.  
XX  
AC ABP97131;  
XX  
DT 24-JUN-2003 (first entry)  
XX  
DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.  
XX  
KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;  
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;  
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;  
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
KW macular degeneration; diabetic retinopathy; cleavage region.  
XX  
OS Homo sapiens.  
XX  
FN WO2003018748-A2.  
XX  
PD 06-MAR-2003.  
XX  
PF 15-AUG-2002; 2002WO-US026319.  
XX  
PR 16-AUG-2001; 2001US-0312726P.  
PR 21-DEC-2001; 2001US-00032376.  
PR 21-MAY-2002; 2002US-00153185.  
XX  
PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.  
XX  
PI Quirk S, Weart IF;  
XX  
WPI; 2003-381408/36.  
XX  
DR Anti-angiogenic composition comprising peptide inhibitor of matrix  
PT metalloproteinase, useful for decreasing the expression of vascular  
PT endothelial growth factor and treating cancers and tissue injuries.  
XX  
PS Claim 17; Page 16; 103pp; English.  
XX  
CC The present invention describes an anti-angiogenic composition (I) for  
CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)  
CC comprises an effective amount of a peptide inhibitor of matrix  
CC metalloproteinase (MMP), where the peptide can inhibit the expression of  
CC VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,  
CC antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (I) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 2  
 ABG76317  
 ID ABG76317 standard; protein; 54 AA.

AC ABG76317;  
 DT 10-MAY-2003 (first entry)  
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #9.  
 KW Human; peptide inhibitor; matrix metalloproteinase-1; MMP-1;  
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnerary.  
 XX Homo sapiens.

OS

XX WO2003016520-A1.

PN 27-FEB-2003.

PD 15-AUG-2002; 2002WO-US026198.

PE 16-AUG-2001; 2001US-0312726P.

PR 21-DEC-2001; 2001US-00032376.

PR 21-MAY-2002; 2002US-00153185.

XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

PA Quirk S, Malik S, Villanueva JM;

PI WPI; 2003-289980/26.

XX Novel peptide inhibitor of proteinase activity of matrix

XX metalloproteinases, e.g. matrix metalloproteinase-2, useful for

PT stimulating cellular proliferation of fibroblasts or keratinocytes.

PT Claim 1; Page 15; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases

XX (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have

CC peptide sequences related to the cleavage regions of the proenzyme forms

CC of the MMPs. The peptide inhibitors are useful for stimulating cellular

CC proliferation of fibroblasts or keratinocytes, promoting healthy skin

CC development, treating wounds, preventing scarring, improving skin tone,

CC reducing wrinkling and for stimulating the development of smooth, healthy

CC skin. The peptide inhibitors are useful as anti-aging and wound healing

CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX

SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 3  
 ADQ17092

ID ADQ17092 standard; peptide; 54 AA.

XX

AC ADQ17092;

DT 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-1 (MMP1) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;

XX human; matrix metalloproteinase; MMP.

XX Homo sapiens.

OS

XX US2004127421-A1.

PN 01-JUL-2004.

PD 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

PR (MALI/) MALIK S.

PA (QUIR/) QUIRK S.

XX Malik S, Quirk S;

PI WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds

XX comprises peptide having sequence related to matrix metalloproteinase

PT proenzyme.

PT Example 1; SEQ ID NO 9; 60pp; English.

PS The present invention provides peptides and compositions containing such

XX peptides that are useful as agents to maintain healthy skin and to

CC promote the condition of the skin. The invention is useful for increasing

CC the amount of fibronectin in tissue. The invention is also useful for

CC encouraging the maintenance and development of healthy skin, preventing

CC and treating wrinkles and for treating wounds. The invention acts as

CC vulnerary and dermatological agents. The present sequence is human matrix

CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in

CC the exemplification of the invention.

XX

SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 8; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

RESULT 4

ADE16002

ID ADE16002 standard; protein; 454 AA.

XX

AC ADE16002;

XX 29-JAN-2004 (first entry)

XX

DE G-coupled protein receptor related polypeptide, SEQ ID No 32.  
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
KW preventive medicine; pharmacogenomics; human.  
XX Homo sapiens.  
XX  
XX W0200283841-A2.  
XX 24-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010713.  
XX  
XX 03-APR-2001; 2001US-0281136P.  
PR 05-APR-2001; 2001US-0281863P.  
PR 05-APR-2001; 2001US-0281906P.  
PR 10-APR-2001; 2001US-0282934P.  
PR 13-APR-2001; 2001US-0283577P.  
PR 13-APR-2001; 2001US-0283578P.  
PR 13-APR-2001; 2001US-0283587P.  
PR 13-APR-2001; 2001US-0283710P.  
PR 17-APR-2001; 2001US-0284234P.  
PR 19-APR-2001; 2001US-0285325P.  
PR 20-APR-2001; 2001US-0285609P.  
PR 23-APR-2001; 2001US-0285748P.  
PR 23-APR-2001; 2001US-0285890P.  
PR 24-APR-2001; 2001US-0286068P.  
PR 27-APR-2001; 2001US-0287213P.  
PR 03-MAY-2001; 2001US-0288509P.  
PR 30-MAY-2001; 2001US-0294495P.  
PR 31-JUL-2001; 2001US-0309216P.  
PR 25-SEP-2001; 2001US-0324775P.  
PR 28-NOV-2001; 2001US-0333900P.  
PR 02-APR-2002; 2002US-00115479.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX WPI; 2003-067574/06.  
DR N-PSDB; ADE16001.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX  
XX Claim 1; SEQ ID NO 32; 320pp; English.  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidaemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
XX Sequence 454 AA;  
SQ

Query Match 100.0%; Score 292; DB 7; Length 454;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFGGLKVTGKPDATLKVWKQPCRCGVPDVAQFVLTGPNRWQTHLYRIEN 54  
DB 50 MQEFGGLKVTGKPDATLKVWKQPCRCGVPDVAQFVLTGPNRWQTHLYRIEN 103  
RESULT 5  
ADE16004  
ID ADE16004 standard; protein; 454 AA.  
XX  
AC ADE16004;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE G-coupled protein receptor related polypeptide, SEQ ID No 34.  
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
KW preventive medicine; pharmacogenomics; human.  
XX  
XX Homo sapiens.  
XX  
XX W0200283841-A2.  
XX  
XX 24-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010713.  
XX  
XX 03-APR-2001; 2001US-0281136P.  
PR 05-APR-2001; 2001US-0281863P.  
PR 05-APR-2001; 2001US-0281906P.  
PR 10-APR-2001; 2001US-0282934P.  
PR 13-APR-2001; 2001US-0283577P.  
PR 13-APR-2001; 2001US-0283578P.  
PR 13-APR-2001; 2001US-0283678P.  
PR 13-APR-2001; 2001US-0283687P.  
PR 13-APR-2001; 2001US-0283710P.  
PR 19-APR-2001; 2001US-0284234P.  
PR 19-APR-2001; 2001US-0285325P.  
PR 20-APR-2001; 2001US-0285609P.  
PR 23-APR-2001; 2001US-0285748P.  
PR 24-APR-2001; 2001US-0285890P.  
PR 27-APR-2001; 2001US-0286068P.  
PR 27-APR-2001; 2001US-0287213P.  
PR 03-MAY-2001; 2001US-0288509P.  
PR 30-MAY-2001; 2001US-0294495P.  
PR 31-JUL-2001; 2001US-0309216P.  
PR 25-SEP-2001; 2001US-0324775P.  
PR 28-NOV-2001; 2001US-0333900P.  
PR 02-APR-2002; 2002US-00115479.  
XX  
XX

us-10-032-376a-9.rag

Mon Nov 15 13:54:01 2004

PA (CURA-) CURAGEN CORP.  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX WPI; 2003-067574/06.  
DR N-PSDB; ADE16008.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX  
XX Claim 1; SEQ ID NO 34; 320pp; English.  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC virucide, fungicide, cytostatic, nootropic, neuroprotective,  
CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
XX Sequence 454 AA;  
XX  
XX Query Match 100.0%; Score 232; DB 7; Length 454;  
XX Best Local Similarity 100.0%; Pred. No. 2e-31;  
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MQEFFGLKVTGKDAETLKVWKPCRCGVPDVAQFVLTEGNPRWEQHLTYYRIEN 54  
XX  
XX 50 MQEFFGLKVTGKDAETLKVWKPCRCGVPDVAQFVLTEGNPRWEQHLTYYRIEN 103  
XX  
XX  
XX RESULT 6  
XX ADE16008  
XX ID ADE16008 standard; protein; 454 AA.  
XX  
XX AC ADE16008;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX G-coupled protein receptor related polypeptide, SEQ ID NO 38.  
XX  
XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
XX virucide; fungicide; cytostatic; nootropic; neuroprotective;  
XX antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;  
XX cell differentiation; cell proliferation; hematopoiesis; wound healing;  
XX angiogenesis; gene therapy; chromosome mapping; tissue typing;  
XX

preventive medicine; pharmacogenomics; human.  
Homo sapiens.  
WO200283841-A2.  
24-OCT-2002.  
03-APR-2002; 2002WO-US010713.  
03-APR-2001; 2001US-0281136P.  
05-APR-2001; 2001US-0281863P.  
05-APR-2001; 2001US-0281906P.  
10-APR-2001; 2001US-0282934P.  
13-APR-2001; 2001US-0283657P.  
13-APR-2001; 2001US-0283678P.  
13-APR-2001; 2001US-0283687P.  
13-APR-2001; 2001US-0283710P.  
17-APR-2001; 2001US-0284234P.  
19-APR-2001; 2001US-0285325P.  
20-APR-2001; 2001US-0285609P.  
23-APR-2001; 2001US-0285748P.  
23-APR-2001; 2001US-0285890P.  
24-APR-2001; 2001US-0286068P.  
27-APR-2001; 2001US-0287213P.  
03-MAY-2001; 2001US-0288509P.  
30-MAY-2001; 2001US-0294495P.  
31-MAY-2001; 2001US-0294801P.  
31-JUL-2001; 2001US-0309216P.  
25-SEP-2001; 2001US-0324775P.  
28-NOV-2001; 2001US-0333900P.  
02-APR-2002; 2002US-00115479.  
(CURA-) CURAGEN CORP.  
Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
WPI; 2003-067574/06.  
N-PSDB; ADE16007.  
New isolated NOVX polypeptides and polynucleotides, useful for  
preventing, diagnosing or treating NOVX-associated disorders e.g.  
diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
Alzheimer's disease, infections.  
Claim 1; SEQ ID NO 38; 320pp; English.  
The invention relates to a novel isolated G-coupled protein receptor  
related polypeptides. The novel polypeptide comprise any of the 22 fully  
defined sequences of 87-1780 amino acids, given in the specification;  
their mature forms; and possible variants. The novel polypeptides have  
the following activities: antidiabetic, anorectic, antibacterial,  
virucide, fungicide, cytostatic, nootropic, neuroprotective,  
antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
receptor related polypeptides are useful in a method of treating or  
preventing in a human, a pathology associated with the G-coupled protein  
receptor related polypeptides. The polypeptides are useful in the  
manufacture of a medicament for treating a syndrome associated with a  
human disease, preferably a NOVX-associated disorder. The novel  
polypeptides are useful for treating, preventing or diagnosing diseases,  
such as metabolic disorders, diabetes, obesity, infectious diseases,  
anorexia, cancer-associated diseases, neurodegenerative disorders,  
Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
disorders, and various dyslipidemias, metabolic disturbances associated  
with obesity, metabolic X syndrome and wasting disorders associated  
chronic diseases and various cancers. The nucleic acids and polypeptides  
may also be used as targets for the identification of small molecules  
that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
therapy, in generation of antibodies that bind immunospecifically to NOVX  
substances for use in therapeutic or diagnostic methods. The nucleic  
acids are further used as hybridization probes, in chromosome mapping,  
tissue typing, preventive medicine, and pharmacogenomics. This sequence  
represents one of the novel G-coupled protein receptor related  
polypeptides of the invention.



CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.

XX Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31; Indels 0; Gaps 0;  
 Matches 54; Conservative 0; Mismatches 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 50 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

# RESULT 7

ADL16006

ID ADE16006 standard; protein; 454 AA.

AC ADE16006;

DT 29-JAN-2004 (first entry)

DE G-coupled protein receptor related polypeptide, SEQ ID No 36.

KW G-coupled protein receptor; anidiabetic; anorectic; antibacterial;  
 KW virucide; fungicide; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; haemostatic; antilipaemic; neurogenesis;  
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
 KW preventive medicine; pharmacogenomics; human.

XX Homo sapiens.

CS

XX WO200283841-A2.

PN

XX 24-OCT-2002.

XX 03-APR-2002; 2002WO-US010713.

XX 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 10-APR-2001; 2001US-0281906P.

PR 13-APR-2001; 2001US-0282934P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283687P.

PR 17-APR-2001; 2001US-0283710P.

PR 19-APR-2001; 2001US-0284234P.

PR 20-APR-2001; 2001US-0285325P.

PR 23-APR-2001; 2001US-0285609P.

PR 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.

PR 24-APR-2001; 2001US-0286068P.

PR 27-APR-2001; 2001US-0287213P.

PR 03-MAY-2001; 2001US-0288509P.

PR 30-MAY-2001; 2001US-0294495P.

PR 31-MAY-2001; 2001US-0294801P.

PR 31-JUL-2001; 2001US-0309216P.

PR 25-SEP-2001; 2001US-0324775P.

PR 28-NOV-2001; 2001US-0333908P.

PR 02-APR-2002; 2002US-00115479.

XX (CURA-) CURAGEN CORP.

XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

PI Voss EZ, Vernet CM, MacDougall JR, Rastelli L, Anderson DW;

PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;

PI

XX

DR WPI; 2003-067574/06.

DR N-PSDB; ADE16005.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 PT Alzheimer's disease, infections.

XX

PS Claim 1; SEQ ID NO 36; 320pp; English.

XX

CC The invention relates to a novel isolated G-coupled protein receptor  
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
 CC defined sequences of 87-1780 amino acids, given in the specification;  
 CC their mature forms; and possible variants. The novel polypeptides have  
 CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaemic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOVX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.

XX Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 50 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

# RESULT 8

ADL93945

ID ADL93945 standard; protein; 454 AA.

XX ADL93945;

AC ADL93945;

XX 20-MAY-2004 (first entry)

DT

XX Human G-coupled protein receptor-related protein #18.

DE

XX

KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;

KW valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;

KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

KW neoplasia; adenocarcinoma; lymphoma; uterus cancer; fertility;

KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

KW Crohn's disease; G-coupled protein receptor; metabolic disorder;

KW neurodegenerative disorder; receptor.

XX

OS	Homo sapiens.	
XX	US2004006205-A1.	
PN	08-JAN-2004.	
XX	02-APR-2002; 2002US-00115479.	
PF	03-APR-2001; 2001US-0281136P.	
XX	05-APR-2001; 2001US-0281863P.	
PR	05-APR-2001; 2001US-0281906P.	
PR	10-APR-2001; 2001US-0282934P.	
PR	13-APR-2001; 2001US-0283657P.	
PR	13-APR-2001; 2001US-0283678P.	
PR	13-APR-2001; 2001US-0283710P.	
PR	17-APR-2001; 2001US-0284234P.	
PR	19-APR-2001; 2001US-0285325P.	
PR	20-APR-2001; 2001US-0285609P.	
PR	23-APR-2001; 2001US-0285748P.	
PR	24-APR-2001; 2001US-0285890P.	
XX	WPI; 2004-224146/21.	
DR	N-PSDB; ADL93944.	
XX		
PI	Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;	
PI	Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;	
PI	Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;	
PI	Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;	
PI	Shimkets RA, Taupier RJ, Edinger S, Mazur A;	
XX		
DR		
DR		
XX		
PT	New G-coupled protein-receptor related polypeptides, for preventing	
PT	treatment or ameliorating, e.g. acquired immunodeficiency syndrome,	
PT	bronchial asthma, Crohn's disease, prostate cancer, hemophilia,	
PT	scleroderma or obesity.	
XX		
PS	Claim 1; Page 68; 220pp; English.	

XX The invention relates to isolated human G-coupled protein receptor-related polypeptides and polynucleotides. The proteins are useful for preventing, treating or ameliorating medical disorders by protein or gene therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect, valve diseases, tuberosus sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, metabolic disorders, neurodegenerative disorders or Crohn's disease. They are also useful as diagnostic or research tools. The present sequence represents a human G-coupled protein receptor-related protein of the invention.

XX SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 8; Length 454;

Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

DB 50 MQEFFGLKVTGKPDATLTKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 103

RESULT 9

ADL93943

ID ADL93943 standard; protein; 454 AA.

XX

AC ADL93943;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human G-coupled protein receptor-related protein #17.

XX

KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;

KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;

KW valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;

KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;

KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

KW Crohn's disease; G-coupled protein receptor; metabolic disorder;

KW neurodegenerative disorder; receptor.

XX OS

XX Homo sapiens.

XX

FN US2004006205-A1.

XX

XX 08-JAN-2004.

XX

XX 02-APR-2002; 2002US-00115479.

XX

XX 03-APR-2001; 2001US-0281136P.

XX

XX 05-APR-2001; 2001US-0281863P.

XX

XX 05-APR-2001; 2001US-0281906P.

XX

XX 10-APR-2001; 2001US-0282934P.

XX

XX 13-APR-2001; 2001US-0283657P.

XX

XX 13-APR-2001; 2001US-0283678P.

XX

XX 13-APR-2001; 2001US-0283710P.

XX

XX 17-APR-2001; 2001US-0284234P.

XX

XX 19-APR-2001; 2001US-0285325P.

XX

XX 20-APR-2001; 2001US-0285609P.

XX

XX 23-APR-2001; 2001US-0285748P.

XX

XX 24-APR-2001; 2001US-0285890P.

PR 27-APR-2001; 2001US-0287213P.  
 PR 03-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 XX  
 PA (LILL/) LI L.  
 PA (GERL/) GERLACH V.  
 PA (LIUX/) LIU X.  
 PA (MILL/) MILLER C E.  
 PA (SPYT/) SPYTEK K A.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (PENA/) PENNA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (ZHON/) ZHONG H.  
 PA (SMIT/) SMITHSON G.  
 PA (CASM/) CASMAN S J.  
 PA (BOLD/) BOLDOGF L.  
 PA (VOSS/) VOSS E Z.  
 PA (VERN/) VERNET C A.  
 PA (MACD/) MACDOUGALL J R.  
 PA (RAST/) RASTELLI L.  
 PA (ZHON/) ZHONG M.  
 PA (MEZE/) MEZES P S.  
 PA (FURT/) FURTA K.  
 PA (PATI/) PATTURAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHIM/) SHIMKETS R A.  
 PA (TAUP/) TAUPIER R J.  
 PA (EDIN/) EDINGER S.  
 PA (MAZU/) MAZUR A.  
 XX  
 PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
 PI Pena CER, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;  
 PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shinkets RA, Taupier RJ, Edinger S, Mazur A;  
 XX  
 DR WPI; 2004-224146/21.  
 DR N-PSDB; ADL93942.  
 XX  
 PT New G-coupled protein-receptor related polypeptides, for preventing  
 PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,  
 PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,  
 PT scleroderma or obesity.  
 XX  
 PS Claim 1; Page 67; 220pp; English.  
 XX  
 CC The invention relates to isolated human G-coupled protein receptor-  
 CC related polypeptides and polynucleotides. The proteins are useful for  
 CC preventing, treating or ameliorating medical disorders by protein or gene  
 CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,  
 CC congenital heart defects, aortic stenosis, atrial septal defect,  
 CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,  
 CC subaortic stenosis, ventricular septal defect, valve diseases, tubercu-  
 CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,  
 CC congenital adrenal hyperplasia, prostate cancer, neoplasm,  
 CC adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia,  
 CC hypercoagulation, idiopathic thrombocytopenic purpura,  
 CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,  
 CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They  
 CC are also useful as diagnostic or research tools. The present sequence  
 CC represents a human G-coupled protein receptor-related protein of the  
 CC invention.  
 XX  
 SQ Sequence 454 AA;  
 Query Match 100.0%; Score 292; DB 8; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 2e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQEFGKLVTKGKPDATILKVMKQRCGVDPVDAQFVLTEGPRWEQTHLYRIEN 54  
 |||||  
 DB 50 MQEFGKLVTKGKPDATILKVMKQRCGVDPVDAQFVLTEGPRWEQTHLYRIEN 103  
 |||||  
 RESULT 10  
 ADL93941  
 ID ADL93941 standard; protein; 455 AA.  
 XX  
 AC ADL93941;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human G-coupled protein receptor-related protein #16.  
 XX  
 KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;  
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;  
 KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;  
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;  
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;  
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;  
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;  
 KW neurodegenerative disorder; receptor.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US2004006205-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 PF 02-APR-2002; 2002US-00115479.  
 XX  
 PR 03-APR-2001; 2001US-0281136P.  
 PR 05-APR-2001; 2001US-0281863P.  
 PR 05-APR-2001; 2001US-0281906P.  
 PR 10-APR-2001; 2001US-0282934P.  
 PR 13-APR-2001; 2001US-0283657P.  
 PR 13-APR-2001; 2001US-0283678P.  
 PR 13-APR-2001; 2001US-0283687P.  
 PR 13-APR-2001; 2001US-0283710P.  
 PR 17-APR-2001; 2001US-0284234P.  
 PR 19-APR-2001; 2001US-0285325P.  
 PR 20-APR-2001; 2001US-0285609P.  
 PR 23-APR-2001; 2001US-0285748P.  
 PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.  
 PR 27-APR-2001; 2001US-0287213P.  
 PR 03-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 PA (LILL/) LI L.  
 PA (GERL/) GERLACH V.  
 PA (LIUX/) LIU X.  
 PA (MILL/) MILLER C E.  
 PA (SPYT/) SPYTEK K A.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (PENA/) PENNA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (ZHON/) ZHONG H.  
 PA (SMIT/) SMITHSON G.  
 PA (CASM/) CASMAN S J.  
 PA (BOLD/) BOLDOGF L.  
 PA (VOSS/) VOSS E Z.  
 PA (VERN/) VERNET C A.

PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (MALY/) MALYANKAR U M.  
PA (SHLM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI Pena CEA, Shenov SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;  
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;  
XX  
XX WPI; 2004-224146/21.  
DR N-PSDB; ADL93940.  
XX  
XX New G-coupled protein-receptor related polypeptides, for preventing  
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,  
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,  
PT scleroderma or obesity.  
XX  
XX Claim 1; Page 67; 220pp; English.

CC The invention relates to isolated human G-coupled protein receptor-  
CC related polypeptides and polynucleotides. The proteins are useful for  
CC preventing, treating or ameliorating medical disorders by protein or gene  
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,  
CC congenital heart defects, aortic stenosis, atrial septal defect,  
CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,  
CC subaortic stenosis, ventricular septal defect, valve diseases, tuberos  
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,  
CC congenital adrenal hyperplasia, prostate cancer, neoplasia,  
CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,  
CC hypercoagulation, idiopathic thrombocytopenic purpura,  
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,  
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They  
CC are also useful as diagnostic or research tools. The present sequence  
CC represents a human G-coupled protein receptor-related protein of the  
CC invention.  
XX  
XX Sequence 455 AA;  
SQ

Query Match 100.0%; Score 292; DB 8; Length 455;  
Best Local Similarity 100.0%; Pred. No. 2e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 50 MQEFFGLKVTGKPDATLTKVMQKPRCGVDPVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 11  
AAB84606  
ID AAB84606 standard; protein; 469 AA.  
XX  
AC AAB84606;  
XX  
DT 05-SEP-2001 (first entry)  
XX  
DE Amino acid sequence of matrix metalloproteinase collagenase 1.  
XX  
XX Growth factor; protein inhibitor; protease; damaged tissue;  
XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
XX keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
XX transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;

KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;  
KW vascular endothelial growth factor; urokinase plasminogen activator;  
KW dermal ulcer; wound.  
XX  
XX Homo sapiens.  
XX WO200149309-A2.  
XX  
XX 12-JUL-2001.  
XX  
XX 21-DEC-2000; 2000WO-1B001935.  
XX  
XX 29-DEC-1999; 99GB-00030768.  
XX  
XX (PFIZ ) PFIZER LTD.  
XX (PFIZ ) PFIZER INC.  
XX  
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;  
XX WPI; 2001-418351/44.  
DR N-PSDB; AAH28221.  
XX  
XX Composition for the treatment of damaged tissue i.e. chronic wounds and  
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth  
PT factor.  
XX  
XX Disclosure; Page 551; 572pp; English.

CC The specification describes a pharmaceutical composition, comprising a  
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent  
CC inhibits the action of at least one specific adverse protein, i.e. a  
CC protease, that is upregulated in a damaged tissue such as a wound  
CC environment. Growth factors which are included in the composition of the  
CC invention are platelet-derived growth factor (PDGF), fibroblast growth  
CC factor (FGF), connective tissue derived growth factor (CTGF), transforming growth factor-beta  
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),  
CC keratinocyte-derived growth factor (KGF), vascular endothelial growth factor (VEGF),  
CC and chrysalin. Inhibitors which are included in the composition of the  
CC invention include inhibitors of urokinase-type plasminogen activator  
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for  
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.  
CC The present sequence represents a human MMP-1, and is used to produce the  
CC composition of the invention  
XX  
XX Sequence 469 AA;  
SQ

Query Match 100.0%; Score 292; DB 4; Length 469;  
Best Local Similarity 100.0%; Pred. No. 2.1e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQEFFGLKVTGKPDATLTKVMQKPRCGVDPVAQFVLTEGNPRWEQTHLYRIEN 54  
DB 67 MQEFFGLKVTGKPDATLTKVMQKPRCGVDPVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 12  
AAE10415  
ID AAE10415 standard; protein; 469 AA.  
XX  
AC AAE10415;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
XX Human matrix metalloproteinase-1 (MMP-1) protein.  
XX  
XX Human; matrix metalloproteinase; MMP-1; hair growth; antisense therapy;  
XX endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1. .19

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FT      20...469
PT      Domain      /label= Mature_MMP_1_protein
FT      90...96
PT      Domain      /label= Cysteine_switch_domain
FT      161...175
PT      /note= "Zinc and calcium binding domain"
XX      WO200166766-A2.
XX      13-SEP-2001.
XX      PD
XX      PD
XX      PF
XX      XX
XX      06-MAR-2001; 2001WO-US007167.
XX      XX
XX      06-MAR-2000; 2000US-0187196P.
XX      XX
XX      (DARW-) DARWIN MOLECULAR CORP.
XX      (SCHA/) SCHATZMAN R.
XX      PA
XX      PI
XX      Fajardo M, Wang K, Smith R, Moss P;
XX      WPI; 2001-582276/65.
XX      DR
XX      XX
XX      Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
PT      proteins encoded by them whose inhibition is useful for modulation of
PT      hair growth in mammals.
XX      PS
XX      Example 2; Fig 3; 119pp; English.
XX      CC
XX      The present sequence is human matrix metalloproteinase (MMP)-1 protein
CC      used in the exemplification of the invention. MMP-25 DNA is located on
CC      chromosome 11q22. Matrix metalloproteinases are a family of zinc
CC      dependent endopeptidases that function extracellularly to degrade
CC      proteins typically found in the extracellular matrix. MMP-25 is expressed
CC      in skin cells of mammals, particularly in breast cells and hair
CC      follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
CC      encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
CC      sample and identifying a sequence that hybridises in the nucleic acid
CC      sample. The identification step involves performing polymerase chain
CC      reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
CC      useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
CC      to modulate hair growth and breast cancer in a mammal
XX      XX
XX      Sequence 469 AA;
XX      Query Match      100.0%; Score 292; DB 4; Length 469;
XX      Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX      Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX      DB      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
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XX      ABU03466
XX      ID      ABU03466 standard; protein; 469 AA.
XX      AC
XX      AC
XX      ABU03466;
XX      DT
XX      21-JAN-2003 (first entry)
XX      DE
XX      Angiogenesis-associated human protein sequence #11.
XX      KW      Human; angiogenesis-associated transcript; angiogenesis;
XX      KW      angiogenesis-associated disease; cancer; cytostatic.
XX      OS
XX      Homo sapiens.
XX      PN      WO200279492-A2.
XX      PD
XX      10-OCT-2002.
XX      XX

PT      14-FEB-2002; 2002WO-US004915.
XX      XX
XX      14-FEB-2001; 2001US-00784356.
XX      PR
XX      22-FEB-2001; 2001US-00791390.
XX      PR
XX      19-APR-2001; 2001US-0285475P.
XX      PR
XX      03-AUG-2001; 2001US-0310025P.
XX      PR
XX      13-NOV-2001; 2001US-0350666P.
XX      PR
XX      29-NOV-2001; 2001US-0334244P.
XX      XX
XX      (EOSB-) EOS BIOTECHNOLOGY INC.
XX      PA
XX      Murray R, Glynn R, Watson SR, Aziz N;
XX      WPI; 2003-040681/03.
XX      DR
XX      N-PSDB; ABX08749.
XX      XX
XX      Detecting angiogenesis-associated transcript in a cell for diagnosing and
PT      treating cancer by contacting a sample with a polynucleotide that
PT      exhibits changes in expression level as a function of time in tissue
PT      undergoing angiogenesis.
XX      PS
XX      Example 2; Page 189; 291pp; English.
XX      CC
XX      The present invention relates to methods and compositions for detecting
CC      an angiogenesis-associated transcript in a cell in a patient. The method
CC      involves contacting a biological sample from the patient with a
CC      polynucleotide that selectively hybridises to a sequence at least 80%
CC      identical to any of the angiogenesis-associated human polynucleotide
CC      sequences given in the specification. These angiogenesis-associated
CC      polynucleotide sequences comprise genes that exhibit changes in
CC      expression levels as a function of time in tissue undergoing
CC      angiogenesis. The method and the polynucleotide sequences of the
CC      invention are useful for diagnosing and treating angiogenesis and
CC      angiogenesis-associated diseases e.g. cancer. The polynucleotide
CC      sequences are also useful in the gene therapy of such disorders. The
CC      angiogenesis-associated proteins encoded by the polynucleotide sequences
CC      are useful as a vaccine for therapeutic and prophylactic immunisation.
CC      ABU03456-ABU03569 represent angiogenesis-associated protein sequences
XX      XX
XX      Sequence 469 AA;
XX      Query Match      100.0%; Score 292; DB 6; Length 469;
XX      Best Local Similarity 100.0%; Pred. No. 2.1e-31;
XX      Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
XX      DB      67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
XX      RESULT 14
XX      ABR58543
XX      ID      ABR58543 standard; protein; 469 AA.
XX      AC
XX      AC
XX      ABR58543;
XX      DT
XX      09-JUL-2003 (first entry)
XX      DE
XX      Human cancer related protein SEQ ID NO:200.
XX      KW      Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX      KW      heart disease; atherosclerosis; endometriosis.
XX      OS
XX      Homo sapiens.
XX      PN      WO2003025138-A2.
XX      PD
XX      27-MAR-2003.
XX      XX
XX      17-SEP-2002; 2002WO-US029560.
XX      PF
XX      17-SEP-2001; 2001US-0323469P.
XX      PR
XX      20-SEP-2001; 2001US-0323887P.
XX      PR

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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:02:10 ; Search time 25.6154 Seconds  
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139.806 Million cell updates/sec

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Perfect score: 292  
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Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/aaa/5B\_COMB.pep: \*  
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6: /cgn2\_6/ptodata/1/aaa/backfiles.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	3	US-08-704-711A-16
2	292	100.0	469	3	US-08-448-489-12
3	292	100.0	469	3	US-09-521-220-16
4	292	100.0	469	3	US-09-391-104-23
5	214	73.3	444	1	US-09-178-002-2
6	214	73.3	466	3	US-08-704-711A-17
7	214	73.3	466	3	US-09-521-220-17
8	214	73.3	467	1	US-09-178-002-4
9	214	73.3	467	3	US-09-391-104-24
10	214	73.3	468	3	US-08-448-489-13
11	189	64.7	476	3	US-08-704-711A-21
12	189	64.7	476	3	US-08-448-489-14
13	189	64.7	476	3	US-09-521-220-21
14	189	64.7	476	3	US-09-391-104-22
15	189	64.7	477	3	US-08-704-711A-20
16	189	64.7	477	3	US-08-448-489-15
17	189	64.7	477	3	US-08-281-313-1
18	189	64.7	477	3	US-09-521-220-20
19	189	64.7	477	3	US-09-391-104-21
20	163	55.8	471	3	US-09-104-002-192
21	163	55.8	513	4	US-10-140-002-132
22	163	55.8	513	4	US-09-862-631-4
23	159	54.5	470	3	US-08-068-392-2
24	159	54.5	470	3	US-08-398-988-2
25	159	54.5	470	3	US-09-391-104-26
26	158	54.1	663	4	US-09-194-468A-30
27	154	52.7	471	4	US-08-994-689C-1

28	151	51.7	264	3	US-09-009-156-6	Sequence 6, Appli
29	151	51.7	264	3	US-09-372-154-6	Sequence 6, Appli
30	151	51.7	267	3	US-08-448-489-18	Sequence 18, Appli
31	151	51.7	267	3	US-09-391-104-27	Sequence 27, Appli
32	151	51.7	271	3	US-08-896-062-2	Sequence 2, Appli
33	150	51.4	135	4	US-09-513-999C-4163	Sequence 4163, Ap
34	147	50.3	471	4	US-08-994-689C-21	Sequence 21, Appli
35	146.5	50.2	920	3	US-09-391-104-7	Sequence 7, Appli
36	144	49.3	462	3	US-08-068-392-3	Sequence 3, Appli
37	144	49.3	462	3	US-08-396-988-3	Sequence 3, Appli
38	144	49.3	631	3	US-08-448-489-17	Sequence 17, Appli
39	144	49.3	660	3	US-08-704-711A-18	Sequence 18, Appli
40	144	49.3	660	3	US-09-521-220-18	Sequence 18, Appli
41	144	49.3	660	3	US-09-391-104-19	Sequence 19, Appli
42	144	49.3	660	4	US-09-317-254-89	Sequence 89, Appli
43	136.5	46.7	604	3	US-09-391-104-30	Sequence 30, Appli
44	136.5	46.7	607	3	US-09-000-041A-2	Sequence 2, Appli
45	136.5	46.7	607	3	US-09-211-704A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1  
US-08-704-711A-16  
; Sequence 16, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILLS, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/704,711A  
; FILING DATE: 20-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/DE95/00957  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 469 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-704-711A-16

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Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
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RESULT 2  
US-08-448-489-12  
; Sequence 12, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SAITO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-12

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
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RESULT 3  
US-09-521-220-16  
; Sequence 16, Application US/09521220  
; Patent No. 6399348  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/09/521,220  
; APPLICATION NUMBER: US/09/521,220  
; FILING DATE: 08-Mar-2000  
; CLASSIFICATION: <Unknown>  
; 21-OCT-1994  
; 17-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/704,711  
; FILING DATE: <Unknown>

APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 469 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-521-220-16

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120  
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RESULT 4  
US-09-391-104-23  
; Sequence 23, Application US/09391104  
; Patent No. 6399371  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Falduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,  
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
; FILE REFERENCE: 6073.US.P1  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; PRIOR FILING DATE: 1997-03-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-23

Query Match 100.0%; Score 292; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 3.8e-31;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54  
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Db 67 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120  
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RESULT 5  
US-09-178-002-2  
; Sequence 2, Application US/09178002  
; Patent No. H001973  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Shou-Ih  
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
; FILE REFERENCE: CGC 2048  
; CURRENT APPLICATION NUMBER: US/09/178,002



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; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match          73.3%; Score 214; DB 1; Length 444;
Best Local Similarity 70.4%; Pred. No. 1.2e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPAETLKWKQRCRGVDPVAQFVLTEGNNRWCTHLTYRIEN 54
DB 43 MQREFGLNVTKGKPAETLDMKKPKRCGVDSGGFMLTPGNPKWERTNLTYSIRN 96

RESULT 6
US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF INVENTIONS: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438839.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-17

Query Match          73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

Query Match          73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRN 119

RESULT 9
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 639371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match          73.3%; Score 214; DB 3; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRN 119

RESULT 10
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloprotease Family
US-08-448-489-13

Query Match          73.3%; Score 214; DB 3; Length 468;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNETLDMKKKPCGVPDGGFMLTGNPKWERTNLTIRN 119

RESULT 11
US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: WO PCT/DE95/00357
; APPLICATION NUMBER:
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-21

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPDATLTKVMKQPCGVPDGGFMLTGNPKWERTNLTIRN 119
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RESULT 12
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motocharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 13
US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6393348
; GENERAL INFORMATION:
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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RESULT 14
US-09-391-104-22
; Sequence 22, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-22

Query Match          64.7%; Score 189; DB 3; Length 476;
Best Local Similarity 63.0%; Pred. No. 3.2e-17;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY      1 MQEFFGLKVTGKPDATLKVMPKQRCGVPDVAQVLTGPNRWEQTHLYRIEN 54
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66 MQKFLGLEVTGKLDTDLEVMKRCGVPDVGHFSSFGMPKWKTKHLYRIYN 119

RESULT 15
US-08-704-711A-20
; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
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us-10-032-376a-9.ra

Mon Nov 15 13:54:01 2004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-20

Query Match 64.7%; Score 189; DB 3; Length 477;  
Best Local Similarity 63.0%; Pred. No. 3.2e-17;  
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
Db 67 MQXFLGLEVTGKLDSDTLEVMKPRCGVPDVGHFRTFPGIPKPKRXTHTLYRIVN 120

Search completed: October 13, 2004, 15:17:05  
Job time : 26.6154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 15:14:50 ; Search time 76.8462 Seconds  
(without alignments)  
226.750 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLKV.....VLTEGNPRWEQHTLTVRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

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2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	292	100.0	54	14	US-10-153-185-9
3	292	100.0	54	14	US-10-219-561-9
4	292	100.0	54	16	US-10-032-376A-9
5	292	100.0	54	15	US-10-335-207-9
6	292	100.0	454	15	US-10-115-479-32
7	292	100.0	454	15	US-10-115-479-34
8	292	100.0	454	15	US-10-115-479-36
9	292	100.0	454	15	US-10-115-479-38
10	292	100.0	469	9	US-09-391-104-23
11	292	100.0	469	9	US-09-801-196-19
12	292	100.0	469	9	US-09-853-386-100
13	292	100.0	469	14	US-10-301-822-119
14	292	100.0	469	14	US-10-021-660-76

15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	14	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	14	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	14	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	14	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appl
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	470	15	US-10-447-315-1	Sequence 1, Appl
27	292	100.0	495	14	US-10-106-698-6283	Sequence 6283, Ap
28	233	79.8	43	14	US-10-219-329-17	Sequence 17, Appl
29	233	79.8	43	14	US-10-153-185-17	Sequence 17, Appl
30	233	79.8	43	14	US-10-219-561-17	Sequence 17, Appl
31	233	79.8	43	16	US-10-032-376A-17	Sequence 17, Appl
32	233	79.8	43	16	US-10-335-207-17	Sequence 17, Appl
33	214	73.3	55	14	US-10-219-329-10	Sequence 10, Appl
34	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
35	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
36	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
37	214	73.3	55	16	US-10-335-207-10	Sequence 10, Appl
38	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
39	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
40	214	73.3	467	10	US-09-759-130B-176	Sequence 176, App
41	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
42	214	73.3	467	16	US-10-741-790-176	Sequence 176, App
43	200.5	68.7	267	14	US-10-133-797-73	Sequence 73, Appl
44	191	65.4	173	15	US-10-115-479-48	Sequence 48, Appl
45	190.5	65.2	325	15	US-10-115-479-78	Sequence 78, Appl

#### ALIGNMENTS

RESULT 1  
US-10-219-329-9  
; Sequence 9, Application US/10219329  
; Publication No. US20030096757A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Weart, Ilona f.  
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds  
; FILE REFERENCE: 1443.035WO1  
; CURRENT APPLICATION NUMBER: US/10/219,329  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-329-9

Query Match 100.0%; Score 292; DB 14; Length 54;  
Best Local Similarity 100.0%; Pred No. 3.8e-30;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLKVMPKQRCGVDPVAFVLTGPNRWEQHTLTVRIEN 54  
Db 1 MQEFFGLKVTGKPDATLKVMPKQRCGVDPVAFVLTGPNRWEQHTLTVRIEN 54

RESULT 2  
US-10-153-185-9  
; Sequence 9, Application US/10153185  
; Publication No. US20030148959A1  
; GENERAL INFORMATION:

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; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-153-185-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
    |||||
Db 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 3
US-10-219-561-9
; Sequence 9, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-219-561-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
    |||||
Db 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 4
US-10-032-376A-9
; Sequence 9, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-376A-9

Query Match      100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
    |||||
Db 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 5
US-10-335-207-9
; Sequence 9, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-335-207-9

Query Match      100.0%; Score 292; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
    |||||
Db 1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54

RESULT 6
US-10-115-479-32
; Sequence 32, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.

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; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 32
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-32
```

```
Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVDPVAQFVLTEGNPRWEQTHLYRIEN 54
Db 50 MQEFFGLKVTGKPDATLKVMPKQPCGVDPVAQFVLTEGNPRWEQTHLYRIEN 103
```

```
RESULT 7
US-10-115-479-34
; Sequence 34, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
```

```
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 34
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-34
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```
Query Match 100.0%; Score 292; DB 15; Length 454;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 MQEFFGLKVTGKPDATLKVMPKQPCGVDPVAQFVLTEGNPRWEQTHLYRIEN 54
Db 50 MQEFFGLKVTGKPDATLKVMPKQPCGVDPVAQFVLTEGNPRWEQTHLYRIEN 103
```

```
RESULT 8
US-10-115-479-36
; Sequence 36, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glenda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
```

; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 36  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;  
Best Local Similarity 100.0%; Pred. No. 4.3e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPDASTLKVMPQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
Db 50 MQEFGKLVTKGKPDASTLKVMPQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 9  
US-10-115-479-36  
; Sequence 38, Application US/10115479  
; Publication No. US20040006205A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Gerlach, Valerie L.  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Zerkhusen, Bryan D.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Boldog, Ferenc L.;  
; APPLICANT: Voss, Edward  
; APPLICANT: Vernet, Corine  
; APPLICANT: MacDougall, John A.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Anderson, David W.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Mezes, Peter S.  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.

; APPLICANT: Malyanker, Uriel M.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: Mazur, Ann  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
; CURRENT APPLICATION NUMBER: US/10/115,479  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 60/281,136  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/281,863  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/281,906  
; PRIOR FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/282,934  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/283,657  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,678  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,687  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/283,710  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/284,234  
; PRIOR FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: 60/285,325  
; PRIOR FILING DATE: 2001-04-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 38  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;  
Best Local Similarity 100.0%; Pred. No. 4.3e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPDASTLKVMPQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
Db 50 MQEFGKLVTKGKPDASTLKVMPQRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103

RESULT 10  
US-09-391-104-23  
; Sequence 23, Application US/09391104  
; Publication No. US20020031817A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Falduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
; FILE REFERENCE: 6073.US.P1  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; PRIOR FILING DATE: 1997-03-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-23

Query Match 100.0%; Score 292; DB 9; Length 469;  
Best Local Similarity 100.0%; Pred. No. 4.5e-29;



```
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 11
US-09-801-196-19
; Sequence 19, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-19

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 12
US-09-853-386-100
; Sequence 100, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NUTR
; TITLE OF INVENTION: Subfamily of Nuclear transcription Factors
; FILE REFERENCE: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HUMAN
US-09-853-386-100

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 13
US-10-301-822-119
```

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; Sequence 119, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-119

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 14
US-10-021-660-76
; Sequence 76, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030152926a1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-76

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.5e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
```

Db 67 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 120

RESULT 15

US-10-308-279-34

; Sequence 34, Application US/10308279

; Publication No. US20030170742A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT

; FILE REFERENCE: D0190 NP

; CURRENT APPLICATION NUMBER: US/10/308,279

; PRIOR FILING DATE: 2002-12-03

; PRIOR APPLICATION NUMBER: 60/337,429

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 34

; LENGTH: 469

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-308-279-34

Query Match 100.0%; Score 292; DB 14; Length 469;

Best Local Similarity 100.0%; Pred. No. 4.5e-29;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 54

Db 67 MQEFGKLVTKGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTTRYEN 120

Search completed: October 13, 2004, 15:35:40

Job time : 77.8462 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:01:19 ; Search time 20.4231 Seconds  
(without alignments)  
254.404 Million cell updates/sec

Title: US-10-032-376A-9  
Perfect score: 292  
Sequence: 1 MQEFGGLKVTGRPDABTLKV.....VLTEGNPRWEQHLTYRIEN 54

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR, 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	468	1 KCRBI	interstitial colla
3	270	92.5	459	1 KCPGI	interstitial colla
4	234	80.1	459	1 KCBGI	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase (EC 3.4.11.1)
6	214	73.3	467	1 KCHUN	neutrophil collage
7	189	64.7	476	1 KCHUS1	stromelysin 2 (EC 3.4.21.2)
8	189	64.7	477	1 KCHUS2	stromelysin 1 (EC 3.4.21.2)
9	186	63.7	478	1 KCRBS1	stromelysin 1 (EC 3.4.21.2)
10	173	59.2	476	1 JC6505	stromelysin 1 (EC 3.4.21.2)
11	173	59.2	477	1 KCMBS1	stromelysin 1 (EC 3.4.21.2)
12	172	58.9	475	1 KCRTH	stromelysin 1 (EC 3.4.21.2)
13	172	58.9	483	2 JC5743	matrix metallopro
14	168	57.5	472	2 S29243	interstitial colla
15	167	57.2	476	1 KCRTS2	stromelysin 2 (EC 3.4.21.2)
16	163	55.8	471	2 A53711	collagenase 3 (EC 3.4.21.2)
17	162	55.5	466	2 A23685	interstitial colla
18	159	54.5	470	2 A24989	metalloelastase
19	158	54.1	663	1 S46492	gelatinase A (EC 3.4.21.2)
20	155	53.1	287	2 A57490	matrilysin (EC 3.4.21.2)
21	151	51.7	267	1 KCHUM	gelatinase A (EC 3.4.21.2)
22	146	50.0	662	2 S70365	gelatinase A (EC 3.4.21.2)
23	144	49.3	462	2 A42401	macrophage elastas
24	144	49.3	660	1 A28153	gelatinase A (EC 3.4.21.2)
25	144	49.3	662	2 A42496	gelatinase A (EC 3.4.21.2)
26	144	49.3	662	2 S34780	gelatinase B (EC 3.4.21.2)
27	135	46.2	708	2 S62507	gelatinase B (EC 3.4.21.2)
28	134.5	46.1	582	2 I38028	matrix metallopro
29	133	45.5	708	2 JCA364	gelatinase B (EC 3.4.21.2)

30	132	45.2	707	1 A34458	gelatinase B (EC 3.4.21.2)
31	130	44.5	707	1 A33796	gelatinase B (EC 3.4.21.2)
32	126.5	43.3	582	2 I84471	matrix metallopro
33	126.5	43.3	669	2 I38029	matrix metallopro
34	126	43.2	712	1 I46031	gelatinase B (EC 3.4.21.2)
35	124	42.5	82	2 PWC052	pro-matrix metallo
36	120.5	41.3	730	1 I52580	gelatinase B (EC 3.4.21.2)
37	120.5	41.3	730	2 JCI456	gelatinase B (EC 3.4.21.2)
38	118.5	40.6	582	2 I48673	matrix metallopro
39	111	38.0	364	2 E71433	probable metallopr
40	108	37.0	341	2 T51957	metalloproteinase
41	108	37.0	342	2 G84885	probable metallopr
42	106.5	36.5	305	2 T08836	probable metallopr
43	103.5	35.4	579	2 T37248	hypothetical prote
44	103.5	35.4	598	2 T32166	probable matrix me
45	100	34.2	521	2 T37252	probable matrix me

ALIGNMENTS

RESULT 1

KCHUI  
N:Interstitial collagenase (EC 3.4.24.7) precursor [validated] - human  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue co  
C:Species: Homo sapiens (man)  
C>Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004  
C:Accession: A37308; S22766; I57620; A00996; A44518; S06132; B60964; S10595; S5  
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St  
Cancer Res. 50, 5431-5437, 1990  
A>Title: Cloning and characterization of human tumor cell interstitial collagenase.  
A:Reference number: A37308; MUID:90352587; PMID:2167156  
A:Accession: A37308  
A:Molecule type: mRNA  
A:Residues: 1-469 <TEM>  
A:Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126  
R:Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.  
J. Clin. Invest. 79, 542-546, 1987  
A>Title: Molecular cloning of human synovial cell collagenase and selection of a single  
A:Reference number: S22766; MUID:87103799; PMID:3027129  
A:Accession: S22766  
A:Molecule type: DNA  
A:Residues: 1-63,65-70 <BRI>  
A:Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667  
R:Angel, P.; Baumann, I.; Stein, B.; Dellus, H.; Rahmsdorf, H.J.; Herrlich, P.  
Mol. Cell. Biol. 7, 2256-2266, 1987  
A>Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene  
A:Reference number: I57620; MUID:87257941; PMID:3037355  
A:Accession: I57620  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-35 <RES>  
A:Cross-references: GB:M1567; NID:G180668; PIDN:AAA52033.1; PID:G180669  
R:Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.  
J. Biol. Chem. 261, 8600-8605, 1986  
A>Title: Human fibroblast collagenase. Complete primary structure and homology to an on  
A:Reference number: A00996; MUID:86196089; PMID:3009463  
A:Accession: A00996  
A:Molecule type: mRNA  
A:Residues: 1-114, 'R', 116-409, 'S', 411-469 <COL>  
A:Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665  
A>Note: part of this sequence was confirmed by protein sequencing of the proenzyme  
R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris  
Biochem. J. 240, 913-916, 1986  
A>Title: Comparison of human stromelysin and collagenase by cloning and sequence analys  
A:Reference number: A90336; MUID:87156645; PMID:3030290  
A:Accession: D29157  
A:Molecule type: mRNA  
A:Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>  
A:Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA28858.1; PID:G38267  
A>Note: parts of this sequence, including the amino end of the proenzyme and of the mat  
R:Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Brown, A.S.; Birkedal-Hansen, H.  
Biochemistry 27, 6751-6758, 1988

Best Local Similarity 100.0%; Pred. No. 2.8e-28;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
DB 67 MOEFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 2

KCRBI  
Interstitial collagenase (EC 3.4.24.7) precursor - rabbit  
N Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
lagenase  
C Species: Oryctolagus cuniculus (domestic rabbit)  
C Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004  
C Accession: A27500; J46694  
R Fini, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.  
Biochemistry 26, 6156-6165, 1987  
A Title: A gene for rabbit synovial cell collagenase: member of a family of metalloprote  
inases  
A Reference number: A27500; MUID:88077876; PMID:2825772  
A Accession: A27500  
A Molecule type: mRNA  
A Residues: 1-468 <PIN>  
A Cross-references: UNIPROT:P13943; GB:M19240  
A Accession: B27500  
A Molecule type: DNA  
A Residues: 1-391;399-468 <FI2>  
A Cross-references: GB:M17820  
A Note: the location of the intron between exons 7 and 8 is approximate  
R Fini, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerho  
ff, C.E.  
Coll. Relat. Res. 6, 239-248, 1986  
A Title: Homology between exon-containing portions of rabbit genomic clones for synovial  
collagenase  
A Reference number: I46694; MUID:87029174; PMID:3021384  
A Accession: I46694  
A Status: translated from GB/EMBL/DDBJ  
A Molecule type: mRNA  
A Residues: 449-468 <FI3>  
A Cross-references: GB:M25663; NID:G531211; PIDN:AAA31203.1; PID:G531212  
C Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th  
e activation peptide.  
C Comment: Procollagenase can be activated without removal of the activation peptide. SE  
quence of the activation peptide is:  
C Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
ch are active.  
C Genetics: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1  
A Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1  
C Function:  
A Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
other proteins  
C Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
nase  
C Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
proteinase  
F 1-18/Domain: signal sequence #status predicted <SIG>  
F 19-468/Product: procollagenase #status predicted <PRO>  
F 19-98/Domain: activation peptide #status predicted <ACT>  
F 59-260/Domain: matrix metalloproteinase homology <MFP>  
F 89-96/Region: autoinhibitory  
F 99-468/Product: interstitial collagenase #status predicted <IAT>  
F 971-465/Domain: hemopexin repeat homology <PXN>  
F 91-217-221-227/Binding site: zinc catalytic (Cys, His, His) (inhibited) #status  
predicted  
F 119-142/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F 117-221-227/Binding site: zinc catalytic (His) (active) #status predicted  
F 218/Active site: Glu #status predicted  
F 277-465/Disulfide bonds: #status predicted

Query Match 96.9%; Score 283; DB 1; Length 468;  
Best Local Similarity 96.3%; Pred. No. 3.6e-27;  
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOEFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
DB 66 MOEFGLKVTGKPDATLTKWKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 119

RESULT 3

KCFGI  
Interstitial collagenase (EC 3.4.24.7) precursor [validated]. pig  
N Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
lagenase

C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: S15986; S33597  
 R;Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.  
 Matrix 11, 161-167, 1991  
 A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of  
 A;Reference number: S15986; MUID:91333421; PMID:1651440  
 A;Accession: S15986  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-469 <RIC>  
 A;Cross-references: UNIPROT:P21692  
 A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by  
 R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.  
 Nucleic Acids Res. 18, 6703, 1990  
 A;Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.  
 A;Reference number: S13597; MUID:91067477; PMID:2174547  
 A;Accession: S13597  
 A;Molecule type: mRNA  
 A;Residues: 25-469 <CLA>  
 A;Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269  
 Submitted to the Brookhaven Protein Data Bank, April 1995  
 R;Li, J.; Brick, P.; Blow, D.M.  
 A;Reference number: A65568; PDB:1FBL  
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466  
 C;Comment: Procollagenase can be activated without removal of the activation peptide. St  
 tion peptide by other proteinases.  
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
 C;Function:  
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
 A;Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-469/Product: procollagenase #status predicted <PRO>  
 F;20-99/Domain: activation peptide #status experimental <ACT>  
 F;100-469/Product: interstitial collagenase #status predicted <MAT>  
 F;272-466/Domain: hemopexin repeat homology <PXN>  
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
 F;219/Active site: Glu #status predicted  
 F;278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;  
 Best Local Similarity 90.7%; Pred. No. 1.5e-25;  
 Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 67 MQEFGKLVTKGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 4  
 KCBOI  
 Interstitial collagenase (EC 3.4.24.7) precursor - bovine  
 N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: S14654; S20336; S14655  
 R;Tamura, M.; Shimokawa, H.; Sasaki, S.  
 submitted to the EMBL Data Library, March 1991  
 A;Reference number: S14654  
 A;Accession: S14654  
 A;Molecule type: mRNA  
 A;Residues: 1-469 <TAM>  
 A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260  
 R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.  
 Arch. Biochem. Biophys. 293, 370-376, 1992  
 A;Title: Purification and characterization of bovine interstitial collagenase and tissue  
 A;Reference number: S20336; MUID:92161820; PMID:1311165  
 A;Accession: S20336

A;Molecule type: protein  
 A;Residues: 19-21,'FP',24-29,'L',31-34,'LL',37-39,'F',86-105,'NPR',109-112,'D',114-125  
 C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in t  
 C;Comment: Procollagenase can be activated without removal of the activation peptide. S  
 tion peptide by other proteinases.  
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of wh  
 C;Function:  
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, an  
 A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
 F;1-18/Domain: signal sequence #status predicted <SIG>  
 F;19-469/Product: procollagenase #status predicted <PRO>  
 F;19-99/Domain: activation peptide #status predicted <ACT>  
 F;60-261/Domain: matrix metalloproteinase homology <MMP>  
 F;90-97/Region: autoinhibitory  
 F;100-469/Product: interstitial collagenase #status predicted <MAT>  
 F;272-466/Domain: hemopexin repeat homology <PXN>  
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
 F;219/Active site: Glu #status predicted  
 F;278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;  
 Best Local Similarity 81.5%; Pred. No. 4.2e-21;  
 Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 67 MQEFGKLVTKGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 5  
 151267  
 collagenase (EC 3.4.24.-) - bullfrog  
 C;Species: Rana catesbeiana (bullfrog)  
 C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C;Accession: I51267  
 R;Corruga, K.; Yomori, S.; Yoshizato, K.  
 Int. J. Dev. Biol. 38, 345-350, 1994  
 A;Title: Regionally and hormonally regulated expression of genes of collagen and collag  
 A;Reference number: I51267; MUID:95071832; PMID:7981043  
 A;Accession: I51267  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-384 <OOP>  
 A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:g913070; PIDN:AAB32661.1; PID:g91307  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
 C;Keywords: hydrolyase; metalloproteinase; zinc; zymogen  
 F;53-231/Domain: matrix metalloproteinase homology <MMP>  
 F;236-381/Domain: hemopexin repeat homology <PXN>  
 F;91,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted  
 F;190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;  
 Best Local Similarity 79.6%; Pred. No. 6.9e-21;  
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MQEFGKLVTKGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54  
 Db 57 LKQFFGLKVTGKPAETLKVYKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 109

RESULT 6  
 KCHUN  
 neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human  
 N;Alternate names: matrix metalloproteinase 8  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32527; S6  
 R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev  
 J. Biol. Chem. 265, 11421-11424, 1990

R;Title: Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.  
 A;Reference number: A37073; MUID:90307647; PMID:2164002  
 A;Accession: A37073  
 A;Molecule type: mRNA  
 A;Residues: 1-467 <HAS>  
 A;Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G180618  
 R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.  
 Blood 77, 2731-2738, 1991  
 A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.  
 A;Reference number: A61175; MUID:91255696; PMID:1646048  
 A;Accession: A61175  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>  
 A;Accession: B61175  
 A;Molecule type: protein  
 A;Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>  
 R;Malliyil, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V  
 Biochemistry 29, 10628-10634, 1990  
 A;Title: Characterization and activation of procollagenase from human polymorphonuclear  
 A;Reference number: S09680; MUID:90249372; PMID:2159879  
 A;Accession: S09680  
 A;Molecule type: protein  
 A;Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-1  
 A;Note: 67-Lys was also found  
 R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
 Biol. Chem. Hoppe-Seyler 371, 733, 1990  
 A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.  
 A;Reference number: S11026; MUID:91000455; PMID:2169766  
 A;Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990  
 A;Accession: S11026  
 A;Molecule type: protein  
 A;Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140, 183-203, 'X', 205-209, 248-261  
 A;Note: 87-Glu was also found  
 R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.  
 Eur. J. Biochem. 202, 1223-1230, 1991  
 A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.  
 A;Reference number: S19576; MUID:92111500; PMID:1662606  
 A;Accession: S19576  
 A;Molecule type: protein  
 A;Residues: 69-103 <BL>  
 R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.  
 FEBS Lett. 313, 59-61, 1992  
 A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procoll  
 A;Reference number: S27225; MUID:93050220; PMID:1330697  
 A;Accession: S27225  
 A;Molecule type: protein  
 A;Residues: 68-103 <BL>  
 R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.  
 Biochem. J. 291, 847-854, 1993  
 A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.  
 A;Reference number: S32527; MUID:93256897; PMID:8489511  
 A;Accession: S32527  
 A;Molecule type: protein  
 A;Residues: 100-112, 263-276 <KN3>  
 R;Knaeuper, V.; Murphy, G.; Tschesche, H.  
 Eur. J. Biochem. 235, 187-191, 1996  
 A;Title: Activation of human neutrophil procollagenase by stromelysin 2.  
 A;Reference number: S62608; MUID:96202934; PMID:8631328  
 A;Accession: S62608  
 A;Molecule type: protein  
 A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>  
 R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.  
 submitted to the Brookhaven Protein Data Bank, January 1994  
 A;Reference number: A67078; PDB:1MNC  
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks,  
 Nat. Struct. Biol. 1, 119-123, 1994  
 A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.  
 A;Reference number: A58274; MUID:95384762; PMID:7656015  
 A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 1  
 C;Comment: This protein is more highly glycosylated than interstitial collagenase and is  
 C;Genetics:  
 A;Gene: GDB:MMP8; CLG1  
 A;Cross-references: GDB:128173; OMIM:120355  
 A;Map position: 11q22.2-11q22.3  
 C;Function:  
 A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous  
 A;Note: cleaves type I collagen most rapidly  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
 C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; n  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-467/Product: procollagenase #status predicted <PRO>  
 F;21-100/Domain: activation peptide #status experimental <ACT>  
 F;59-263/Domain: matrix metalloproteinase homology <MMP>  
 F;89-96/Region: autoinhibitory  
 F;101-467/Product: neutrophil collagenase #status predicted <MAT>  
 F;273-464/Domain: hemopexin repeat homology <PXN>  
 F;54, 73, 112, 119, 204, 246/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;73-74/Cleavage site: Asp-Met (autolytic) #status experimental  
 F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental  
 F;91, 217, 221, 227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
 F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental  
 F;167, 169, 182, 195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experime  
 F;174, 175, 177, 179, 197, 200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e  
 F;174, 221, 227/Binding site: zinc, catalytic (His) (active) #status experimental  
 F;218/Active site: Glu #status predicted  
 F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental  
 F;279-464/Disulfide bonds: #status predicted  
 Query Match 73.3%; Score 214; DB 1; Length 467;  
 Best Local Similarity 70.4%; Pred. No. 1.2e-18;  
 Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MQRFGLKVTGKPDATLTKVMKPRGVPDVAQFVLTEGPRWEOPHLTYRIN 54  
 Db 66 MQRFGLNVTGKNEETLDMKAPRGVDPDSGGFMTLPNGKWRNTLYRIN 119  
 RESULT 7  
 KCHUS2  
 stromelysin 2 (EC 3.4.24.22) precursor [validated] - human  
 N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C;Accession: A28816; A47496  
 R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach,  
 Biochem. J. 253, 187-192, 1988  
 A;Title: The collagenase gene family in humans consists of at least four members.  
 A;Reference number: A90339; MUID:88339885; PMID:2844164  
 A;Accession: A28816  
 A;Molecule type: mRNA  
 A;Residues: 1-476 <NUL>  
 A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36629  
 A;Note: mRNA for this protein was detected in several human tumors  
 R;Wondor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-  
 J. Biol. Chem. 268, 17341-17347, 1993  
 A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gen  
 A;Reference number: A47496; MUID:93352520; PMID:8349617  
 A;Accession: A47496  
 A;Molecule type: protein  
 A;Residues: 17-33 <WIN>  
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
 C;Genetics:  
 A;Gene: GDB:MMP10; STMY2  
 A;Cross-references: GDB:120392; OMIM:185260  
 A;Map position: 11q22.3-11q23  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

Biochemistry 37, 4699-4702, 1998  
A>Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (Q)  
A:Reference number: A58912; MUID:9548733; PMID:9545733  
A:Contents: annotation  
R:Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, February 1997  
A:Reference number: A68466; PDB:1HFS  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160  
R:Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.  
Protein Sci. 4, 1966-1976, 1995  
A>Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain au  
A:Reference number: A58914; MUID:96117647; PMID:8535233  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms  
R:Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.; Es  
Biochemistry 30, 6476-6483, 1991  
A>Title: Human fibroblast stromelysin catalytic domain: expression, purification, and c  
A:Reference number: A39589; MUID:91274298; PMID:1647201  
A:Contents: annotation  
R:Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, August 1995  
A:Reference number: A66637; PDB:1SLM  
A:Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47/57-267  
R:Gooley, P.R.; O'connell, J.F.  
submitted to the Brookhaven Protein Data Bank, March 1995  
A:Reference number: A67284; PDB:2BRT  
A:Contents: annotation; conformation by (1)H-NMR, residues 100-272  
R:Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Es  
Biochemistry 32, 13098-14008, 1993  
A>Title: Secondary structure and zinc ligation of human recombinant short-form stromely  
A:Reference number: A58915; MUID:94059987; PMID:8241164  
A:Contents: annotation; conformation by (1)H-NMR  
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation  
C:Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of wh  
C:Genetics:  
A:Gene: GDB:MMP3; STMV; STMV1  
A:Cross-references: GDB:I20727; OMIM:185250  
A:Map position: 11q23-11q23  
C:Function:  
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s  
A>Note: degrades various extracellular matrix proteins, including fibronectin, plasmino  
plasminogen to yield a fragment with angiostatin activity  
C:Superfamily: interstitial collagenase; hemoexin repeat homology; matrix metalloprote  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-477/Product: prostomelysin 1 #status experimental <PRO>  
F:18-99/Domain: activation peptide #status experimental <ACT>  
F:60-264/Domain: matrix metalloproteinase homology <MMP>  
F:100-477/Product: stromelysin 1 #status experimental <MAT>  
F:284-477/Domain: hemoexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:120/Binding site: carbonylcarate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
F:219/Active site: Glu #status predicted  
F:290-477/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 477;  
Best Local Similarity 63.0%; Pred. No. 1.6e-15;  
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

OY 1 MQFFGLKVTGKDPAETLKYNKPRCGVPDVAQFVLTEGNRPWQTHTLYRIEN 54  
| | | | | : | | | | | : | | | | | : | | | | |  
DB 67 MQFELGLEVTGKLSDTLEWKRRCGVDPVGHPTRTPGGIPKWRKTHLYRIVN 120  
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 9  
KCRES1  
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); p  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C:Accession: A37306; A29157  
R:Finzi, M.B.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckhoff,  
Arthritis Rheum. 30, 1254-1264, 1987





## RESULT 12

KCR2IH

stromelysin 1 (EC 3.4.24.17) precursor - rat  
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro-  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text\_change 09-Jul-2004  
C:Accession: A00997; PS0150; S22767  
R:Matrisian, L.M.; Glazchenhua, N.; Gesnel, M.C.; Breathnach, R.  
EMBO J. 4, 1435-1440, 1985  
A:Title: Epidermal growth factor and oncogenes induce transcription of the same cellular  
A:Reference number: A00997; MUID:85284930; PMID:3875482  
A:Accession: A00997  
A:Molecule type: mRNA  
A:Residues: 1-475 <MAT>  
A:Cross-references: UNIPROT:P03957; GB:X02601; NID:X02601; PIDN:CAA26448.1; PID:G57461  
R:Uemishi, F.; Yasumitsu, H.; Ahsida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.  
J. Biochem. 108, 537-543, 1990  
A:Title: Purification and properties of extracellular matrix-degrading metallo-proteinase  
A:Reference number: PS0150; MUID:91154156; PMID:1963430  
A:Accession: PS0150  
A:Molecule type: protein  
A:Residues: 19-20,'X', 22-28;110-112,'X', 114-115,'X', 117,'X', 119;309-325 <UME>  
R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.  
Nucleic Acids Res. 15, 1139-1151, 1987  
A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a  
A:Reference number: A26403; MUID:87146421; PMID:3547333  
A:Contents: annotation; introns  
A:Note: Intron positions were determined by comparison of the previously reported cDNA s  
R:Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.  
J. Biol. Chem. 263, 11892-11899, 1988  
A:Title: Structure-function relationships in the collagenase family member transin.  
A:Reference number: S22767; MUID:8829869; PMID:2841336  
A:Contents: annotation; active site; activation  
A:Note: molecules with mutations in the autoinhibitory region showed a much increased te  
A:Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme  
R:Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.  
J. Biol. Chem. 266, 1584-1590, 1991  
A:Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon  
A:Reference number: A43028; MUID:91107652; PMID:1988438  
A:Contents: annotation; autoinhibitory region  
A:Note: Arg-89 and Cys-92 are essential for maintaining latency  
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wi  
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation  
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi  
C:Genetics:  
A:Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1  
C:Function:  
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-475/Product: prostromelysin 1 #status predicted <PRO>  
F:18-97/Domain: activation peptide #status predicted <ACT>  
F:58-262/Domain: matrix metalloproteinase homology <MMP>  
F:88-95/Region: autoinhibitory  
F:98-475/Product: stromelysin 1 #status predicted <MAT>  
F:282-475/Domain: hemopexin repeat homology <PXN>  
F:90,216,220,226/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:216,220,226/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:217/Active site: zinc, catalytic (His) (active) #status predicted  
F:288-475/Disulfide bonds: #status predicted

Query Match 58.9%; Score 172; DB 1; Length 475;

Best Local Similarity 53.7%; Pred. No. 2e-13;

Matches 29; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 65 MQKFLGLKLVTKGKLDNTMLMKRPGCVDPVGGFTFGSPKRWKKNHISYRIVN 118

## RESULT 13

JCS743

matrix metalloproteinase (EC 3.4.24.-) precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 09-Dec-1997 #sequence\_revision 23-Jan-1998 #text\_change 09-Jul-2004  
C:Accession: JCS743  
R:Bartlett, J.D.; Simmer, J.P.; Xue, J.; Margolis, H.C.; Moreno, E.C.  
Gene 183, 123-128, 1996  
A:Title: Molecular cloning and mRNA tissue distribution of a novel matrix metalloprotei  
A:Reference number: JCS743; MUID:97149288; PMID:8996096  
A:Accession: JCS743  
A:Molecule type: mRNA  
A:Residues: 1-483 <BAR>  
A:Cross-references: UNIPROT:P79287; GB:U54825; NID:G1800212; PIDN:AAB41396.1; PID:G1800  
A:Experimental source: enamel organ  
C:Comment: This enzyme plays a role in enamel biomineralization and development.  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: hydrolase; metalloproteinase; zinc  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-483/Product: matrix metalloproteinase #status predicted <MAT>  
F:68-271/Domain: matrix metalloproteinase homology <MMP>  
F:280-483/Domain: hemopexin repeat homology <PXN>  
F:100,226,230,236/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:226,230,236/Binding site: zinc, catalytic (His) #status predicted  
F:227/Active site: Glu #status predicted

Query Match 58.9%; Score 172; DB 2; Length 483;

Best Local Similarity 59.6%; Pred. No. 2e-13;

Matches 31; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRI 52

Db 75 LQAFFGLRVTKGLDRTMDVIKRCGCPDVAANYRIFPGSPKWKKNLTLYRI 126

## RESULT 14

S29243

interstitial collagenase (EC 3.4.24.7) precursor - mouse  
N:Alternate names: matrix metalloproteinase 1 (MMP1)  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Nov-1993 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: S29243  
R:Henriet, P.; Rousseau, G.G.; Beckhout, Y.  
FEBS Lett. 310, 175-178, 1992  
A:Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat  
A:Reference number: S29243; MUID:93011910; PMID:1383028  
A:Accession: S29243  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-472 <HEN>  
C:Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G5360  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F:65-268/Domain: matrix metalloproteinase homology <MMP>  
F:279-472/Domain: hemopexin repeat homology <PXN>  
F:97,223,227,233/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F:223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted  
F:224/Active site: Glu #status predicted

Query Match 57.5%; Score 168; DB 2; Length 472;

Best Local Similarity 57.4%; Pred. No. 6.2e-13;

Matches 31; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 72 MQSFFGLVTKGLDPTDIMRXRCGCPDVAANYRIFPGSPKWKKNLTLYRIYN 125

## RESULT 15

KCR2S2

stromelysin 2 (EC 3.4.24.22) precursor - rat



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 110.769 Seconds  
(without alignments)  
280.495 Million cell updates/sec

Title: US-10-032-376a-9

Perfect score: 292

Sequence: 1 MOEFFGLKVTGKPDATLKV.....VLTEGNPRWEQHTLVRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:\*

1: uniprot\_prot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292	100.0	469	1 MM01_HUMAN	P03956 homo sapien
2	292	100.0	469	2 AAP3520	AAP3520 homo sapi
3	283	96.9	468	1 MM01_RABIT	P13943 cryctolagus
4	279	95.5	469	1 MM01_HORSE	Q9xsz5 equus cabal
5	270	92.5	469	1 MM01_PIG	P21692 sus scrofa
6	234	80.1	469	1 MM01_BOVIN	P28053 bos taurus
7	231.5	79.3	384	1 MM01_RANCA	Q11133 rana catesb
8	214	73.3	467	1 MM08_HUMAN	P22894 homo sapien
9	204	69.9	205	2 Q810Z2	Q810Z2 mus musculu
10	204	69.9	463	2 Q9EPL6	Q9EPL6 mus musculu
11	204	69.9	464	2 Q9EPL5	Q9EPL5 mus musculu
12	196	67.1	466	1 MM08_RAT	Q88766 rattus norv
13	189	64.7	476	1 MM10_HUMAN	P09238 homo sapien
14	189	64.7	476	2 AAP36110	AAP36110 homo sapi
15	189	64.7	477	1 MM03_HUMAN	P08254 homo sapien
16	189	64.7	477	2 AAH63676	AAH63676 homo sapi
17	189	64.7	477	2 AAH69716	AAH69716 homo sapi
18	189	64.7	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
19	189	64.7	478	2 AAO63580	AAO63580 canis fam
20	186	63.7	145	2 Q9N283	Q9N283 bos taurus
21	186	63.7	393	2 Q8MI18	Q8MI18 felis silve
22	186	63.7	478	1 MM03_RABIT	P28863 cryctolagus
23	184	63.0	252	2 Q6FWQ3	Q6FWQ3 xenopus lae
24	184	63.0	252	2 AAT00547	AAT00547 xenopus lae
25	184	63.0	259	2 Q7ZTI9	Q7ZTI9 xenopus lae
26	183	62.7	472	2 Q93342	Q93342 gallus gall
27	183	62.7	477	1 MM03_HORSE	Q28397 equus cabal
28	181	62.0	466	2 Q7SYX1	Q7SYX1 xenopus lae
29	180	61.6	269	2 Q7SZT5	Q7SZT5 xenopus lae
30	179	61.3	458	2 Q6DCN8	Q6DCN8 xenopus lae
31	178	61.0	258	2 Q75ZS8	Q75ZS8 xenopus lae

32	178	61.0	259	2 Q6DF35	Q6DF35 xenopus tro
33	178	61.0	481	1 MM20_BOVIN	O18767 bos taurus
34	176	60.3	465	2 Q8C209	Q8C209 mus musculu
35	176	60.3	465	2 Q8C230	Q8C230 mus musculu
36	176	60.3	465	2 AAH42742	AAH42742 mus muscu
37	176	60.3	465	2 BAC40805	BAC40805 mus muscu
38	176	60.3	471	1 MM13_RABIT	O52805 cryctolagus
39	174	59.6	167	2 Q7ZWD0	Q7ZWD0 brachydanic
40	174	59.6	482	1 MM20_MOUSE	P57748 mus musculu
41	173	59.2	476	1 MM10_MOUSE	O55123 mus musculu
42	173	59.2	477	1 MM03_MOUSE	P28862 mus musculu
43	173	59.2	479	2 Q922W6	Q922W6 mus musculu
44	172	58.9	475	1 MM03_RAT	P03957 rattus norv
45	172	58.9	483	1 MM20_HUMAN	O50882 homo sapien

#### ALIGNMENTS

RESULT 1  
MM01\_HUMAN  
ID MM01\_HUMAN STANDARD; PRT; 469 AA.  
AC P03956; P08156;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
metalloproteinase-1) (MMP-1) (Fibroblast collagenase).  
GN Name=MMP1; Synonyms=CLG;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90352587; PubMed=2167156;  
RA Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,  
RA Stetler-Stevenson W.G.;  
RT "Cloning and characterization of human tumor cell interstitial  
collagenase."  
RL Cancer Res. 50:5431-5437(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87156645; PubMed=3030290;  
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,  
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
RT "Comparison of human stromelysin and collagenase by cloning and  
sequence analysis."  
RL Biochem. J. 240:913-916(1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86196089; PubMed=3009463;  
RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,  
RA Eisen A.Z.;  
RT "Human fibroblast collagenase. Complete primary structure and homology  
to an oncogene transformation-induced rat protein."  
RL J. Biol. Chem. 261:6600-6605(1986).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
RA Heller R., Davis R.W.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [16]  
RN SEQUENCE OF 1-35 FROM N.A.  
RP MEDLINE=87257941; PubMed=3037355;  
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,  
RA Herrlich P.,  
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human  
RT collagenase gene is mediated by an inducible enhancer element located  
RT in the 5'-flanking region.";  
RL Mol. Cell. Biol. 7:2256-2266 (1987).  
RN [7]  
RN SEQUENCE OF 1-70 FROM N.A.  
RP TISSUE=Synovial cell.  
RC MEDLINE=87109799; PubMed=2557822;  
RA Brinckerhoff C.E., Ruby P.L., Ausin S.D., Fini M.E., White H.D.;  
RT "Molecular cloning of human synovial cell collagenase and selection of  
RT a single gene from genomic DNA.";  
RL J. Clin. Invest. 79:542-546 (1987).  
RN [8]  
RN SEQUENCE OF 100-112 AND 270-287.  
RP TISSUE=Fibroblast;  
RC MEDLINE=90104231; PubMed=2557822;  
RA Clark I.M., Cawston T.E.;  
RT "Fragments of human fibroblast collagenase. Purification and  
RT characterization.";  
RL Biochem. J. 263:201-206 (1989).  
RN [9]  
RN SIMILARITY TO THERMOLYSIN TYPE PROTEASES.  
RP MEDLINE=87194799; PubMed=3032950;  
RA McKerrow J.H.;  
RT "Human fibroblast collagenase contains an amino acid sequence  
RT homologous to the zinc-binding site of Serratia protease.";  
RL J. Biol. Chem. 262:5943-5943 (1987).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.  
RP MEDLINE=95394760; PubMed=7656013;  
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,  
RA Brown P.A., Johnson W.H., Murray E.J.;  
RT "Structure of the catalytic domain of human fibroblast collagenase  
RT complexed with an inhibitor.";  
RL Nat. Struct. Biol. 1:106-110 (1994).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.  
RP MEDLINE=94304829; PubMed=8031754;  
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;  
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase  
RT complexed to itself.";  
RL Biochemistry 33:8207-8217 (1994).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.  
RP MEDLINE=94105765; PubMed=8278810;  
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,  
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,  
RA Jordan S.R.;  
RT "Structure of the catalytic domain of fibroblast collagenase complexed  
RT with an inhibitor.";  
RL Science 263:375-377 (1994).  
RN [13]  
RN X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.

RX MEDLINE=94377426; PubMed=8090713;  
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,  
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;  
RT "1.56-A structure of mature truncated human fibroblast collagenase.";  
RL Proteins 19:98-109 (1994).  
RN [14]  
RN STRUCTURE BY NMR OF 101-269.  
RP MEDLINE=98145213; PubMed=9484219;  
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,  
RA Powers R.;  
RT "High-resolution solution structure of the inhibitor-free catalytic  
RT fragment of human fibroblast collagenase determined by  
RT multidimensional NMR.";  
RL Biochemistry 37:1495-1504 (1998).  
CC -I- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
CC the helical domain. Also cleaves collagens of types VII and X.  
CC -I- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
CC collagen. Cleavage of the triple helix of collagen at about three-  
CC quarters of the length of the molecule from the N-terminus, at  
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
CC substrates and alpha-macroglobulins at bonds where p1' is a  
CC hydrophobic residue.  
CC -I- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -I- ENZYME REGULATION: Can be activated without removal of the  
CC activation peptide.  
CC -I- DOMAIN: There are two distinct domains in this protein; the  
CC catalytic N-terminal, and the C-terminal which is involved in  
CC substrate specificity and in binding TIMP (tissue inhibitor of  
CC metalloproteinases).  
CC -I- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and  
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22  
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form  
CC can act as activator for collagenase.  
CC -I- SIMILARITY: Belongs to peptidase family M10A.  
CC -I- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
EMBL; X05231; CAA28858.1; -;  
EMBL; M13509; AAA35699.1; -;  
EMBL; M16567; AAA52033.1; -;  
EMBL; U78045; AAB36941.1; -;  
EMBL; BC013875; AAH13875.1; -;  
EMBL; M15996; AAA35700.1; -;  
EMBL; X54925; CAA35691.1; -;  
PIR; A37308; KCHUI.  
PDB; 1AYK; NMR; @=101-269.  
PDB; 1CGE; X-ray; @=102-269.  
PDB; 1CGF; X-ray; A/B=102-263.  
PDB; 1CGL; X-ray; A/B=101-269.  
PDB; 1HFC; X-ray; @=101-269.  
PDB; 2AYK; NMR; @=101-269.  
PDB; 2ICL; X-ray; @=101-269.  
PDB; 3AYK; NMR; A=101-269.  
PDB; 4AYK; NMR; A=101-269.  
MEROPS; M10.001; -;  
GlycoSuiteDB; P03956; -;  
Genew; HGNC:7155; MWPI.  
MIM; 120353; -;  
GO; GO:0008433; F:collagenase activity; TAS.  
GO; GO:0008270; F:zinc ion binding; TAS.  
GO; GO:0006508; P:proteolysis and peptidolysis; TAS.  
InterPro; IPR000585; Hemopexin.  
InterPro; IPR006026; Peptidase M.  
InterPro; IPR001818; Pept\_M10A\_M12B.  
InterPro; IPR006025; Pept\_M\_2n\_BS.  
InterPro; IPR009070; PGSD\_like.

[illegible]

"Homology between exon-containing portions of rabbit genomic clones for synovial cell collagenase and human foreskin and synovial cell mRNA".  
Coll. Relat. Res. 6:239-248(1986).  
-!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.  
-!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.  
-!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).  
-!- ENZYME REGULATION: Can be activated without removal of the activation peptide.  
-!- SIMILARITY: Belongs to peptidase family M10A.  
-!- SIMILARITY: Contains 1 hemopexin-like domain.

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EMBL; M17823; AAB88016.1; JOINED.  
EMBL; M17820; AAB88016.1; JOINED.  
EMBL; M17821; AAB88016.1; JOINED.  
EMBL; M17822; AAB88016.1; JOINED.  
EMBL; M19240; AAB88016.1; JOINED.  
EMBL; M25663; AAA31203.1; -.  
PIR; A27500; KCRL.  
HSSP; F03956; ICGL.  
MEROPS; M10.001; -.  
InterPro; IPRO00585; Hemopexin.  
InterPro; IPRO06026; Peptidase M.  
InterPro; IPRO01818; Pept\_M10A\_M12B.  
InterPro; IPRO06025; Pept\_M\_Zn\_BS.  
InterPro; IPRO09070; PGSD\_like.  
Pfam; PF00045; Hemopexin; 4.  
Pfam; PF00413; Peptidase M10; 1.  
Pfam; PF03933; Peptidase M10\_N; 1.  
PRINTS; PR00138; MATRXIN.  
SMART; SM00120; HX; 4.  
SMART; SM00235; ZnMG; 1.  
PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
PROSITE; PS00024; HEMOPEXIN; 1.  
PROSITE; PS00142; ZINC\_PROTEASE; 1.  
Calcium-binding; Collagen degradation; Extracellular matrix;  
Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
Zymogen.

SIGNAL 1  
PROPEP 19  
CHAIN 99  
DOMAIN 274  
SITE 91  
METAL 123  
METAL 123  
METAL 157  
METAL 167  
METAL 169  
METAL 169  
METAL 174  
METAL 175  
METAL 177  
METAL 179  
METAL 182  
METAL 189  
METAL 191

Activation peptide.  
Interstitial collagenase.  
Hemopexin-like.  
Cysteine switch (potential).  
Calcium 1 (By similarity).  
Calcium 2 (By similarity).  
Zinc 1 (By similarity).  
Zinc 1 (By similarity).  
Calcium 3 (By similarity).  
Calcium 3 (via carbonyl oxygen) (By similarity).  
Calcium 3 (via carbonyl oxygen) (By similarity).  
Calcium 3 (via carbonyl oxygen) (By similarity).  
Zinc 1 (By similarity).  
Calcium 2 (via carbonyl oxygen) (By similarity).  
Calcium 2 (via carbonyl oxygen) (By similarity).

RT RT Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase\_M10; 1.  
  
Query Match 100.0%; Score 292; DB 1; Length 469;  
Best Local Similarity 100.0%; Pred. No. 8.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MQEFGKLVGTGPDAETLKVMKQPCRGVDPDVAQFVLTEGNPRWEOHTLTTRYEN 54  
Db 67 MQEFGKLVGTGPDAETLKVMKQPCRGVDPDVAQFVLTEGNPRWEOHTLTTRYEN 120  
  
RESULT 2  
AAP35520 PRELIMINARY; PRT; 469 AA.  
AC AAP35520;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Matrix metalloproteinase 1 (Interstitial collagenase).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RS SEQUENCE FROM N.A.  
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.  
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
RT vector."  
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BT006874; AAP35520.1; -.  
KW Collagen.  
SQ SEQUENCE 469 AA; 54007 MW; 4B1361DCF4C54B20 CRC64;  
  
Query Match 100.0%; Score 292; DB 2; Length 469;  
Best Local Similarity 100.0%; Pred. No. 8.2e-29;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MQEFGKLVGTGPDAETLKVMKQPCRGVDPDVAQFVLTEGNPRWEOHTLTTRYEN 54  
Db 67 MQEFGKLVGTGPDAETLKVMKQPCRGVDPDVAQFVLTEGNPRWEOHTLTTRYEN 120  
  
RESULT 3  
MM01 RABIT STANDARD; PRT; 468 AA.  
ID MM01 RABIT  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
DE metalloproteinase-1) (MMP-1).  
GN Name=MMP1;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxId=9986;  
RN [1]  
RS SEQUENCE FROM N.A.  
RA Tissue-Synovial cell.  
RC MEDLINE=88077876; PubMed=2825772;  
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;  
RT "A gene for rabbit synovial cell collagenase: member of a family of  
RT metalloproteinases that degrade the connective tissue matrix.";  
RL Biochemistry 26:6156-6165(1987).  
RN [2]  
RS SEQUENCE OF 449-468 FROM N.A.  
RC STRAIN=New Zealand white;  
RA MEDLINE=87029174; PubMed=3021384;  
RX Fini M.E., Austin S.D., Hoit P.T., Ruby P.L., Gross R.H., White H.D.,  
RA Brinckerhoff C.E.;

FT	METAL	193	193	similarity).	CC
FT	METAL	195	195	Calcium 2 (By similarity).	DR
FT	METAL	197	197	Zinc 1 (By similarity).	DR
FT	METAL	198	198	Calcium 3 (By similarity).	DR
FT	METAL	200	200	Calcium 1 (By similarity).	DR
FT	METAL	217	217	Calcium 3 (By similarity).	DR
FT	METAL	218	218	Zinc 2 (catalytic) (By similarity).	DR
FT	ACT SITE	221	221	By similarity.	DR
FT	METAL	221	221	Zinc 2 (catalytic) (By similarity).	DR
FT	METAL	227	227	Zinc 2 (catalytic) (By similarity).	DR
FT	METAL	227	227	Calcium 4 (via carbonyl oxygen) (By	DR
FT	METAL	284	284	similarity).	DR
FT	METAL	328	328	Calcium 4 (via carbonyl oxygen) (By	DR
FT	METAL	377	377	similarity).	DR
FT	METAL	377	377	Calcium 4 (via carbonyl oxygen) (By	DR
FT	METAL	426	426	similarity).	DR
FT	METAL	426	426	Calcium 4 (via carbonyl oxygen) (By	DR
FT	CARBOHYD	119	119	similarity).	DR
FT	DISULFID	277	277	N-linked (GlcNAc. . .) (Probable).	KW
FT	SEQUENCE	468	468	By similarity.	KW
SQ	SEQUENCE	468	468	DA90538919952B8C CRC64;	SQ
Query Match 96.9%; Score 283; DB 1; Length 468;					
Best Local Similarity 96.3%; Pred. No. 1.2e-27;					
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	1	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	54		
DB	66	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	119		
RESULT 4					
MM01	HORSE	STANDARD;	PRT;	469	AA.
ID	MM01	HORSE			
AC	QXK575;				
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	03-JUL-2004	(Rel. 44, Last annotation update)			
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix				
DE	metalloproteinase-1) (MMP-1).				
GN	Names=MMPI;				
OS	Equus caballus (Horse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
CX	NCBI_TaxID=9796;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Richardson D.W.;				
RT	"Cloning and expression of equine matrix metalloproteinase 1				
RL	(Interstitial collagenase)."				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: Cleaves collagens of types I, II, and III at one site in				
CC	the helical domain. Also cleaves collagens of types VII and X.				
CC	-1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native				
CC	collagen. Cleavage of the triple helix of collagen at about three-				
CC	quarters of the length of the molecule from the N-terminus, at				
CC	775-Gly- -Ile-776 in the alpha-1(I) chain. Cleaves synthetic				
CC	substrates and alpha-macroglobulins at bonds where P1' is a				
CC	hydrophobic residue.				
CC	-1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By				
CC	similarity).				
CC	-1- ENZYME REGULATION: Can be activated without removal of the				
CC	activation peptide.				
CC	-1- SIMILARITY: Belongs to peptidase family M10A.				
CC	-1- SIMILARITY: Contains 1 hemopexin-like domain.				
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).					
-----					
CC	1	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	54		
DB	67	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	120		
RESULT 5					
MM01	PIG				
Query Match 95.5%; Score 279; DB 1; Length 469;					
Best Local Similarity 94.4%; Pred. No. 3.9e-27;					
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	1	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	54		
DB	67	MOEFFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN	120		
RESULT 5					
MM01	PIG				

ID AC P21692; STANDARD; PRT; 469 AA.  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
 metalloproteinase-1) (MMP-1).  
 GN Name=MMP1;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 CX NCBI\_TaxID=9923;  
 [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=91333421; PubMed=1651440;  
 RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;  
 RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and  
 modulation of expression of RNA in vitro by various cytokines.";  
 RL Matrix 11:161-167(1991).  
 [2]  
 RP SEQUENCE OF 25-469 FROM N.A.  
 RX TISSUE=Synovial cell;  
 RC MEDLINE=91047477; PubMed=2174547;  
 RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;  
 RT "Nucleotide sequence of a cDNA for porcine type I collagenase,  
 obtained by PCR.";  
 RL Nucleic Acids Res. 18:6703-6703(1990).  
 [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.  
 RX MEDLINE=96173003; PubMed=8590015;  
 RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,  
 RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;  
 RT "Structure of full-length porcine synovial collagenase reveals a C-  
 terminal domain containing a calcium-linked, four-bladed beta-  
 propeller.";  
 RL Structure 3:541-549(1995).  
 [4]  
 RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.  
 RX MEDLINE=95142615; PubMed=7840605;  
 RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,  
 RA O'Hare M.C.;  
 RT "Recombinant porcine collagenase: purification and autolysis.";  
 RL Arch. Biochem. Biophys. 316:123-127(1995).  
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
 the helical domain. Also cleaves collagens of types VII and X.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 collagen. Cleavage of the triple helix of collagen at about three-  
 quarters of the length of the molecule from the N-terminus, at  
 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 substrates and alpha-macroglobulins at bonds where P1' is a  
 hydrophobic residue.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
 CC -!- ENZYME REGULATION: Can be activated without removal of the  
 activation peptide.  
 CC -!- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment  
 having reduced collagenolytic activity.  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL; X54724; CAA38526.1; -;  
 CC PIR; S15986; KCPGI.  
 CC DR MEROPS; M10.001; -;  
 CC InterPro; IPR000595; Hemopexin.  
 CC InterPro; IPR006026; Peptidase\_M.

DR InterPro; IPR001818; Pept\_M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGBD-like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.  
 DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00138; MATRXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZnMC; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KW 3D-structure: Autocatalytic cleavage; Calcium-binding;  
 KW Collagen degradation; Direct protein sequencing; Extracellular matrix;  
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;  
 KW Zymogen.  
 FT SIGNAL 1 19  
 FT CHAIN 20 99 Activation peptide.  
 FT CHAIN 100 469 Interstitial collagenase.  
 FT CHAIN 100 258 18 kDa interstitial collagenase.  
 FT DOMAIN 275 469 Hemopexin-like.  
 FT SITE 92 92 Cysteine switch (Potential).  
 FT SITE 258 259 Cleavage (autolytic).  
 FT METAL 124 124 Calcium 1.  
 FT METAL 158 158 Calcium 2.  
 FT METAL 168 168 Zinc 1.  
 FT METAL 170 170 Zinc 1.  
 FT METAL 175 175 Calcium 3.  
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen).  
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen).  
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen).  
 FT METAL 183 183 Zinc 1.  
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen).  
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen).  
 FT METAL 194 194 Calcium 2.  
 FT METAL 196 196 Zinc 1.  
 FT METAL 198 198 Calcium 3.  
 FT METAL 199 199 Calcium 1.  
 FT METAL 201 201 Calcium 3.  
 FT METAL 218 218 Zinc 2 (catalytic).  
 FT ACT\_SITE 219 219 Zinc 2 (catalytic).  
 FT METAL 222 222 Zinc 2 (catalytic).  
 FT METAL 228 228 Calcium 4 (via carbonyl oxygen).  
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen).  
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen).  
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen).  
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen).  
 FT DISULFID 278 466  
 FT CARBOHYD 120 120  
 FT STRAND 101 102 N-linked (GlcNAc...) (Potential).  
 FT TURN 104 105  
 FT STRAND 113 118  
 FT TURN 123 124  
 FT TURN 127 142  
 FT TURN 143 144  
 FT STRAND 148 152  
 FT STRAND 159 164  
 FT STRAND 182 184  
 FT TURN 190 193  
 FT STRAND 195 198  
 FT TURN 199 200  
 FT STRAND 204 204  
 FT STRAND 211 211  
 FT HELIX 212 223  
 FT TURN 224 225  
 FT STRAND 226 227  
 FT TURN 232 233  
 FT TURN 235 236  
 FT TURN 250 260  
 FT HELIX 277 278  
 FT TURN 280 281  
 FT STRAND 286 290  
 FT TURN 291 292







MM08 HUMAN  
ID MM08 HUMAN STANDARD; PRT; 467 AA.  
AC P22894;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix  
DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).  
GN Name=MMP8; Synonyms=CLG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCB TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90307647; PubMed=2164002;  
RA Hasty K.A., Pourmotabed T.F., Goldberg G.I., Thompson J.P.,  
RA Spinelletto D.G., Stevens R.M., Mainardi C.L.;  
RT "Human neutrophil collagenase. A distinct gene product with homology  
RT to other matrix metalloproteinases.";  
RL J. Biol. Chem. 265:11421-11424 (1990).  
RN [2]  
RN SEQUENCE OF 21-140.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90249372; PubMed=2159879;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RT "Characterization and activation of procollagenase from human  
RT polymorphonuclear leukocytes. N-terminal sequence determination of the  
RT proenzyme and various proteolytically activated forms.";  
RL Eur. J. Biochem. 189:295-300 (1990).  
RN [3]  
RN SEQUENCE OF 21-103.  
RC TISSUE=Neutrophils;  
RX MEDLINE=92111500; PubMed=162606;  
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;  
RT "Mercurial activation of human polymorphonuclear leucocyte  
RT procollagenase.";  
RL Eur. J. Biochem. 202:1223-1230 (1991).  
RN [4]  
RN SEQUENCE OF 85-120, AND CHARACTERIZATION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91104978; PubMed=2176876;  
RA Mallva S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,  
RA Birksdal-Hansen H., van Wart H.E.;  
RT "Characterization of 58-kilodalton human neutrophil collagenase:  
RT comparison with human fibroblast collagenase.";  
RL Biochemistry 29:10628-10634 (1990).  
RN [5]  
RN PARTIAL SEQUENCE.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90380298; PubMed=2169256;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";  
RL Biol. Chem. Hoppe-Seyler 371:295-304 (1990).  
RN [6]  
RN ERRATUM.  
RX MEDLINE=91000455; PubMed=2169766;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RL Biol. Chem. Hoppe-Seyler 371:733-733 (1990).  
RN [7]  
RN CYSTEINE-SWITCH MECHANISM.  
RC TISSUE=Neutrophils;  
RX MEDLINE=93050220; PubMed=1330697;  
RA Blaesser J., Triebel S., Reinke H., Tschesche H.;  
RT "Formation of a covalent Hg-Cys-bond during mercurial activation of  
RT PMNL procollagenase gives evidence of a cysteine-switch mechanism.";  
RL FEBS Lett. 313:59-61 (1992).  
RN [8]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.  
RX MEDLINE=94185631; PubMed=8137810;  
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;  
RT "The X-ray crystal structure of the catalytic domain of human  
RT neutrophil collagenase inhibited by a substrate analogue reveals the

essentials for catalysis and specificity.";  
RL EMBO J. 13:1263-1269 (1994).  
RN [9]  
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.  
RX MEDLINE=94139930; PubMed=8307185;  
RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,  
RA Tschesche H., Bode W.;  
RT "Structural implications for the role of the N terminus in the  
RT 'superactivation' of collagenases. A crystallographic study.";  
RL FEBS Lett. 338:227-233 (1994).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.  
RX MEDLINE=95384762; PubMed=7656015;  
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,  
RA Qoronfleh M.W., Banks T.M., Rubin B.;  
RT "Structure of human neutrophil collagenase reveals large S1'  
RT specificity pocket.";  
RL Nat. Struct. Biol. 1:119-123 (1994).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.  
RX MEDLINE=97390108; PubMed=9249047;  
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,  
RA Bode W., Gomis-Rueth F.-X.;  
RT "1.8-A crystal structure of the catalytic domain of human neutrophil  
RT collagenase (matrix metalloproteinase-8) complexed with a  
RT peptidomimetic hydroxamate primed-side inhibitor with a distinct  
RT selectivity profile.";  
RL Eur. J. Biochem. 247:356-363 (1997).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.  
RX MEDLINE=98318039; PubMed=9655333;  
RA Brandstetter H., Eng R.A., von Roeder E.G., Moroder L., Huber R.,  
RA Bode W., Grams F.;  
RT "Structure of malonic acid-based inhibitors bound to human neutrophil  
RT collagenase. A new binding mode explains apparently anomalous data.";  
RL Protein Sci. 7:1303-1309 (1998).  
CC -1- FUNCTION: Can degrade fibrillar type I, II, and III collagens.  
CC -1- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the  
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves  
CC type III collagen more slowly than type I.  
CC -1- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.  
CC -1- ENZYME REGULATION: Cannot be activated without removal of the  
CC activation peptide.  
CC -1- SUBCELLULAR LOCATION: Stored in intracellular granules.  
CC -1- TISSUE SPECIFICITY: Neutrophils.  
CC -1- SIMILARITY: Belongs to peptidase family M10A.  
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC ENBL; J05556; AAA88021.1; --  
CC FR; A37073; KCHUN.  
CC PDB; 1A85; X-ray; A=105-262.  
CC PDB; 1A86; X-ray; A=105-262.  
CC PDB; 1B2S; X-ray; A=99-263.  
CC PDB; 1I73; X-ray; A=100-262.  
CC PDB; 1I76; X-ray; A=100-262.  
CC PDB; 1JAN; X-ray; A=99-262.  
CC PDB; 1JAC; X-ray; A=100-262.  
CC PDB; 1JAP; X-ray; A=100-262.  
CC PDB; 1JQA; X-ray; A=100-262.  
CC PDB; 1JH1; X-ray; A=105-262.  
CC PDB; 1JH9; X-ray; A=100-262.  
CC PDB; 1KBC; X-ray; A=100-262.  
CC PDB; 1MMB; X-ray; A=100-262.  
CC PDB; 1MNC; X-ray; A=101-263.  
CC MEROPS; M10.002; --

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DR Genew: HGNC:7175; MWP8.
DR MIM: 120355;
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0008130; F:neutrophil collagenase activity; TAS.
DR GO: GO:0008270; F:zinc ion binding; TAS.
DR GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR009070; PGSD_like.
DR Pfam: PF00045; Hemopexin; 4.
DR Pfam: PF00413; Peptidase_M10; 1.
DR PRINTS: PR00138; MATRIXIN.
DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE: PS00024; HEMOPEXIN; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 100 Activation peptide.
FT CHAIN 101 467 Neutrophil collagenase.
FT DOMAIN 276 467 Hemopexin-like.
FT SITE 91 91 Cysteine switch.
FT METAL 157 157 Calcium 1.
FT METAL 167 167 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2.
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Calcium 2 (via carbonyl oxygen).
FT METAL 189 189 Zinc 1.
FT METAL 191 191 Calcium 1.
FT METAL 193 193 Calcium 1 (via carbonyl oxygen).
FT METAL 193 193 Calcium 1.
FT METAL 193 193 Zinc 1.
FT METAL 197 197 Calcium 2.
FT METAL 200 200 Calcium 2.
FT METAL 217 217 Zinc 2 (catalytic).
FT ACT_SITE 218 218 Zinc 2 (catalytic).
FT METAL 221 221 Zinc 2 (catalytic).
FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
FT METAL 286 286 similarity).
FT METAL 378 378 Calcium 3 (via carbonyl oxygen) (By
FT METAL 425 425 similarity).
FT METAL 425 425 Calcium 3 (via carbonyl oxygen) (By
FT METAL 425 425 similarity).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Probable).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 8.9e-19;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFLGLKVTGKPDATLKVMPKQRCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 54
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66 MQEFLGLKVTGKPDATLKVMPKQRCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 119

RESULT 9
Q81022 PRELIMINARY; PRT; 205 AA.
AC Q81022;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-like B (Fragment).

```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RX [1]_
RP SEQUENCE FROM N.A.
RC STRAIN:129/SvJ;
RA Brachwaite M., Waelz P., Nagaraja R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY211543; AAO37584.1; -.
DR MEROPS; M10.034; -.
DR GO: GO:0005578; C:extracellular matrix; IEA.
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR009070; PGSD_like.
DR Pfam: PF00413; Peptidase_M10; 1.
DR PRINTS: PR00138; MATRIXIN.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Collagen.
FT NON_TER 205
FT SIGNAL 205 205
SQ SEQUENCE 205 AA; 23403 MW; DBD1E974E8769643 CRC64;

Query Match 69.9%; Score 204; DB 2; Length 205;
Best Local Similarity 66.7%; Pred. No. 7.2e-18;
Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFLGLKVTGKPDATLKVMPKQRCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 54
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64 MQEFLGLKVTGKPDATLKVMPKQRCGVDPVDAQFVLTEGNPRWEOTHLTYRIEN 117

RESULT 10
Q9EPL6 PRELIMINARY; PRT; 463 AA.
AC Q9EPL6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative matrix metalloproteinase.
GN Name=Mmp1b; Synonyms=McolB;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=21167837; PubMed=1113146;
RA Balbin M., Fuyo A., Knauper V., Lopez J.M., Alvarez J., Sanchez L.M.,
RA Quesada V., Bordallo J., Murphy G., Lopez-Otin C.;
RT "Identification and enzymatic characterization of two diverging murine
RT counterparts of human interstitial collagenase (MMP-1) expressed at
RT sites of embryo implantation."
RL J. Biol. Chem. 276:10253-10262(2001).
DR EMBL; AJ278461; CAC18879.1; -.
DR HSSP; P08254; 1HV7.
DR MEROPS; M10.034; -.
DR MGD; MGI:1933847; Mmp1b.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR InterPro: IPR000585; Hemopexin.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001843; Pept_M10A_M10C.
DR InterPro: IPR001818; Pept_M10A_M12B.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam; PF02051; Fragilysin; 1.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.

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DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix  
DE metalloproteinase-8) (MMP-8).  
GN Name=Mmp8;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Lewis;  
RA Overall C.M., Lowne D., Wells G., Burel S., Clements J.M.;  
RA "Cloning, expression, characterization and activation properties of  
FT rat neutrophil collagenase (MMP-8).";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.  
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the  
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves  
CC type III collagen more slowly than type I.  
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By  
CC similarity).  
CC -!- ENZYME REGULATION: Cannot be activated without removal of the  
CC activation peptide (By similarity).  
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AJ007288; CAA07432.1; -  
CC HSSP: P22894; 1BZS.  
CC MROPS; M10.002; -  
CC InterPro: IPR000585; Hemopexin.  
CC InterPro: IPR001819; Pept M10A\_M12B.  
CC InterPro: IPR006025; Pept M.Zn.BS.  
CC InterPro: IPR009070; PGSD-like.  
CC Pfam: PF00045; Hemopexin; 4.  
CC Pfam: PF00413; Peptidase M10; 1.  
CC PRINTS: PR00138; MAIRIXIN.  
CC PROSITE: PS00546; CYSTEINE\_SWITCH; 1.  
CC PROSITE: PS00142; ZINC\_PROTEASE; 1.  
CC Calcium-binding; Collagen degradation; 1.  
CC Glycoprotein; Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc;  
CC Zymogen.  
FT SIGNAL 1 20 By similarity.  
FT PROPEP 21 101 Activation peptide (By similarity).  
FT CHAIN 102 465 Neutrophil collagenase.  
FT DOMAIN 277 466 Hemopexin-like.  
FT SITE 92 92 Cysteine switch (By similarity).  
FT METAL 158 158 Calcium 1 (By similarity).  
FT METAL 168 168 Zinc 1 (By similarity).  
FT METAL 170 170 Zinc 1 (By similarity).  
FT METAL 175 175 Calcium 2 (By similarity).  
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 183 183 Zinc 1 (By similarity).  
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 194 194 Calcium 1 (By similarity).  
FT METAL 196 196 Zinc 1 (By similarity).

FT METAL 199 199 Calcium 2 (By similarity).  
FT METAL 201 201 Calcium 2 (By similarity).  
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).  
FT ACT\_SITE 219 219 By similarity.  
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).  
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).  
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By  
FT similarity).  
FT DISULFID 280 465 Probable.  
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;  
Query Match 67.1%; Score 196; DB 1; Length 466;  
Best Local Similarity 63.0%; Pred. No. 1.8e-16;  
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MQEFGKLVTKGKPAETLVKVKQRCGVPDVAQFVLTGPNRWQTHLTYPRIEN 54  
DB 67 MQEFGKLVTKGKPAETLVKVKQRCGVPDVAQFVLTGPNRWQTHLTYPRIEN 120  
RESULT 13  
WM10\_HUMAN STANDARD; PRT; 476 AA.  
ID WM10\_HUMAN  
AC P09238;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)  
DE (MMP-10) (Transin-2) (SL-2).  
DE Name=MMP10; Synonyms=STMY2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8833985; PubMed=2844164;  
RA Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.,  
RA Brethnach R.;  
RT "The collagenase gene family in humans consists of at least four  
RT members.";  
RL Biochem. J. 253:187-192(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.L., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,

CC and V; weakly collagens III, IV, and V. Activates procollagenase.  
CC -1- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on  
CC collagen types III, IV and V is weak.  
CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).  
CC -1- SIMILARITY: Belongs to peptidase family M10A.  
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC -----  
CC EMBL; X07820; CAA30679.1; -.  
CC EMBL; BC002591; AAO02591.1; -.  
CC FIR; A28816; KCHUS2.  
CC HSSP; P08254; 1G05.  
CC MEROPS; M10.006; -.  
CC Genew; HGNC:7156; MMP10.  
CC MIM; 185260; -.  
CC GO; GO:000578; C:extracellular matrix; TAS.  
CC GO; GO:0005615; C:extracellular space; TAS.  
CC GO; GO:0004222; F:metalloendopeptidase activity; TAS.  
CC GO; GO:0008270; F:zinc ion binding; TAS.  
CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.  
CC InterPro; IPR000585; Hemopexin.  
CC InterPro; IPR006026; Hemopexin.  
CC InterPro; IPR001818; Pept\_M10A\_M12B.  
CC InterPro; IPR006025; Pept\_M10A\_BS.  
CC InterPro; IPR009070; PGSD-like.  
CC Pfam; PF00413; Peptidase M10; 1.  
CC Pfam; PF03933; Peptidase M10\_N; 1.  
CC PRINTS; PR00138; MATRIXIN.  
CC SMART; SM00120; HX; 4.  
CC SMART; SM00235; ZnMc; 1.  
CC PROSITE; PS00546; CYSTEINE SWITCH; 1.  
CC PROSITE; PS00024; HEMOPEXIN; 1.  
CC PROSITE; PS00142; ZINC PROTEASE; 1.  
CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;  
KW Metalloprotease; signal; zinc; zymogen.  
FT SIGNAL 1 17 Probable.  
FT PROPEP 18 98 Activation peptide.  
FT CHAIN 99 476 Stromelysin-2.  
FT DOMAIN 286 476 Hemopexin-like.  
FT SITE 91 91 Cysteine switch (By similarity).  
FT METAL 217 217 Zinc (catalytic) (By similarity).  
FT ACT\_SITE 218 218 By similarity.  
FT METAL 221 221 Zinc (catalytic) (By similarity).  
FT METAL 227 227 Zinc (catalytic) (By similarity).  
FT DISULFID 289 476 By similarity.  
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDFEF92A0D6 CRC64;  
  
Query Match 64.7%; Score 189; DB 1; Length 476;  
Best Local Similarity 63.0%; Pred.No. 1.5e-15;  
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 MQBFFGLKVTGKPDATLTKVMKQPCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 66 MQKFLGLEVTGKLDTDLTLEVMKPCGVDPDVGHFSSFFGMPKWKTHLYRIYN 119  
  
RESULT 14  
ID AAP36110 PRELIMINARY; PRT; 476 AA.  
AC AAP36110;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Matrix metalloproteinase 10 (stromelysin 2).  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kainline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RT "Cloning of human full-length cDNAs in BD Creator (TM) System Donor  
RT vector".  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BT007442; AAP36110.1; -.  
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDFEF92A0D6 CRC64;  
  
Query Match 64.7%; Score 189; DB 2; Length 476;  
Best Local Similarity 63.0%; Pred.No. 1.5e-15;  
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 MQBFFGLKVTGKPDATLTKVMKQPCGVDPDVAQFVLTGPNRWEQTHLYRIEN 54  
Db 66 MQKFLGLEVTGKLDTDLTLEVMKPCGVDPDVGHFSSFFGMPKWKTHLYRIYN 119  
  
RESULT 15  
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AC P08254;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)  
DE (MMP-3) (Transin-1) (SL-1).  
GN Name=MMP3; Synonyms=STMY1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.  
RX MEDLINE=88198243; PubMed=3360803;  
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,  
RA Kurkinen M.;  
RT "The complete primary structure of human matrix metalloproteinase-3.  
RT Identity with stromelysin.";  
RL J. Biol. Chem. 263:6742-6745 (1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=87156645; PubMed=3030290;  
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,  
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
RT "Comparison of human stromelysin and collagenase by cloning and  
RT sequence analysis.";  
RL Biochem. J. 240:913-916 (1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88016164; PubMed=3477804;  
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,  
RA Grant G.A., Bauer E.A., Goldberg G.I.;  
RT "Human skin fibroblast stromelysin: structure, glycosylation,  
RT substrate specificity, and differential expression in normal and  
RT tumorigenic cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
RA Heller R., Davis R.W.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Posl C.L., Yi Q.,

RA Nickerson D.A.;  
RT "SeattleSNP. NHLBI HL6682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
[6]  
RN  
RP ZYMOGEN ACTIVATION  
RX MEDLINE=90344802; PubMed=2383557;  
RA Nagase H., Enghild J.J., Suzuki K., Salvesen G.;  
RT "Stepwise activation mechanisms of the precursor of matrix metalloproteinase 3 (stromelysin) by proteinases and (4-aminophenyl)mercuric acetate.";  
RT Biochemistry 29:5783-5789(1990).  
[7]  
RN  
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.  
RX MEDLINE=95384761; PubMed=7656014;  
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P., Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P., Johnson B.A.;  
RT "The NMR structure of the inhibited catalytic domain of human stromelysin-1.";  
RL Nat. Struct. Biol. 1:111-118(1994).  
[8]  
RN  
RP STRUCTURE BY NMR OF 100-267.  
RX MEDLINE=99043696; PubMed=9827994;  
RA Stockman B.J., Walton D.J., Gates J.A., Scallill T.A., Klooterman D.A., Myszak S.A., Jacobsen E.J., Belongia K.L., Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A., Ledbetter S.R., Kaytes P.S., Vogel G., Marshall V.P., Petzold G.L., Fooman R.A.;  
RT "Solution structures of stromelysin complexed to thiazidazole inhibitors.";  
RL Protein Sci. 7:2281-2286(1998).  
[9]  
RN  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.  
RX MEDLINE=96117647; PubMed=855233;  
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J., Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K., Hermes J.D., Springer J.P.;  
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic domain and of the C-truncated proenzyme.";  
RL Protein Sci. 4:1966-1976(1995).  
[10]  
RN  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.  
RX MEDLINE=96311273; PubMed=8740360;  
RA Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F., Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;  
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin catalytic domain and its comparison with members of the zinc metalloproteinase superfamily.";  
RL Structure 4:375-386(1996).  
[11]  
RN  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.  
RX MEDLINE=97236965; PubMed=9083493;  
RA Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L., Girotta N.N., Kopka I.E., Ianza T.J., Levorse D.A., Maccoss M., Owens K.A., Ponnipom M.M., Simson J.P., Harrison R.K., Nledwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J., McDonnell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M., Shen F., Colletti A., Krieter P.A., Hagmann W.K.;  
RT "Inhibition of stromelysin-1 (MMP-3) by Pl'-biphenyllylethyl carboxylalkyl dipeptides.";  
RL J. Med. Chem. 40:1026-1040(1997).  
[12]  
RN  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH TIMP1.  
RX MEDLINE=97433330; PubMed=9288970;  
RA Gomis-Rueh F.-X., Maskos K., Betz M., Bergner A., Huber R., Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P., Bartunik H., Bode W.;  
RT "Mechanism of inhibition of the human matrix metalloproteinase stromelysin-1 by TIMP-1.";  
RL Nature 389:77-81(1997).  
[13]  
RN  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.  
RX MEDLINE=99005562; PubMed=9792098;  
RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W., Trepoed C.M., Mott J.E., Marshall V.P., Petzold G.L., Poorman R.A., O'Sullivan T.J., Schostarez H.J., Mitchell M.A.;  
RT "Structural characterizations of nonpeptidic thiazidazole inhibitors of matrix metalloproteinases reveal the basis for stromelysin selectivity.";  
RL Protein Sci. 7:2118-2126(1998).  
[14]  
RN  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.  
RX MEDLINE=20013067; PubMed=10543949;  
RA Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M., Barnett B.J.;  
RT "Crystal structure of the stromelysin catalytic domain at 2.0-A resolution: inhibitor-induced conformational changes.";  
RL J. Mol. Biol. 293:545-557(1999).  
[15]  
RN  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.  
RX MEDLINE=99349695; PubMed=10422833;  
RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwein D.F., Johnson L.L., Purchase C.F. II, White A.D., Dhanaraj V., Roth B.D., Johnson L.L., Hupe D., Humblet C., Blundell T.L.;  
RT "X-ray structure of human stromelysin catalytic domain complexed with nonpeptide inhibitors: implications for inhibitor selectivity.";  
RL Protein Sci. 8:1455-1462(1999).  
[16]  
RN  
RP STRUCTURE BY NMR OF 100-272.  
RX MEDLINE=98434377; PubMed=9760240;  
RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.;  
RT "Solution structure of the catalytic domain of human stromelysin-1 complexed to a potent, nonpeptidic inhibitor.";  
RL Biochemistry 37:14048-14056(1998).  
CC  
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I, III, IV, and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase.  
CC  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where Pl', P2' and P3' are hydrophobic residues.  
CC  
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC  
CC -!- SIMILARITY: Contains 1 hemoxepin-like domain.  
CC  
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DR EMBL; X05232; CAA28859.1; -  
DR EMBL; J03209; AAA36321.1; -  
DR EMBL; U78045; AAB36942.1; -  
DR EMBL; AF405705; AAK95247.1; -  
DR PIR; A28156; KCHUS1.  
DR PDB; 1B3D; X-ray; A/B=100-272.  
DR PDB; 1B8Y; X-ray; A=100-266.  
DR PDB; 1B1W; X-ray; A/B=100-272.  
DR PDB; 1BM6; NMR; @=100-272.  
DR PDB; 1BQO; X-ray; A/B=100-272.  
DR PDB; 1C3I; X-ray; A/B=100-272.  
DR PDB; 1C8T; X-ray; A/B=103-269.  
DR PDB; 1CAQ; X-ray; A=100-287.  
DR PDB; 1CIZ; X-ray; A=100-267.  
DR PDB; 1CQR; X-ray; A/B=100-272.  
DR PDB; 1D5J; X-ray; A/B=100-272.  
DR PDB; 1D7X; X-ray; A/B=100-272.  
DR PDB; 1D8F; X-ray; A/B=100-272.  
DR PDB; 1D8M; X-ray; A/B=100-272.  
DR PDB; 1G05; X-ray; A/B=100-272.  
DR PDB; 1G49; X-ray; A/B=100-272.  
DR PDB; 1G4K; X-ray; A/B/C=100-267.  
DR PDB; 1HFS; X-ray; @=105-264.

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DR  PDB; 1HY7; X-ray; A/B=100-272.
DR  PDB; 1MIW; Model; A=100-268.
DR  PDB; 1OO9; NMR; A=100-267.
DR  PDB; 1QIA; X-ray; A/B/C/D=106-267.
DR  PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR  PDB; 1SLM; X-ray; @=18-272.

Query Match      64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred. No. 1.5e-15;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY      1 MQEPPGLKVTGKPDATLKMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
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Search completed: October 13, 2004, 15:14:41  
Job time : 111.769 secs



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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:57:16 ; Search time 104.359 Seconds  
(without alignments)  
189.060 Million cells updates/sec

Title: US-10-032-376A-10  
Perfect score: 307  
Sequence: 1 MRRFFGLNVTKPNEETLDX.....LTPGNPKWERTNLTIRRY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	307	100.0	55	8	ADQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AB84610 Amino aci
6	307	100.0	467	4	AAE10416 Human mat
7	307	100.0	467	4	AAE10416 Human neu
8	307	100.0	467	6	ABG5358 Human neu
9	307	100.0	467	8	ABO32581 Secreted
10	226	73.6	454	8	ADQ10212 Human pol
11	221	72.0	454	8	ADL93947 Human G-c
12	221	72.0	454	7	ADE16002 G-coupled
13	221	72.0	454	7	ADE16008 G-coupled
14	221	72.0	454	7	ADE16006 G-coupled
15	221	72.0	454	8	ADL93945 Human G-c
16	221	72.0	454	8	ADL93943 Human G-c
17	221	72.0	455	8	ADL93941 Human G-c
18	221	72.0	469	4	AAE10415 Human aci
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20	221	72.0	469	6	ABU03466 Angiogene
21	221	72.0	469	6	ABR58843 Human can
22	221	72.0	469	6	ABR58842 Human can
23	221	72.0	469	6	ABR48148 Human bla
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25	221	72.0	469	6	ABU56597 Lung can

26	221	72.0	469	6	ABU07454	Abu07454 Protein d
27	221	72.0	469	6	ABP54454	Abp54454 Matrix me
28	221	72.0	469	7	ADB79176	Abd79176 Matrix me
29	221	72.0	469	7	AD334550	Ade34550 Human skl
30	221	72.0	469	7	AD316000	Ade16000 G-coupled
31	221	72.0	469	7	AD316010	Ade16010 G-coupled
32	221	72.0	469	7	AD339849	Adn39849 Cancer/an
33	221	72.0	469	7	AD338694	Adn38694 Cancer/an
34	221	72.0	469	7	AD338696	Adn38696 Cancer/an
35	221	72.0	469	7	AD339850	Adn39850 Cancer/an
36	221	72.0	469	7	AD395538	Adn95538 Human BEC
37	221	72.0	469	8	AD393949	Adl93949 Human G-c
38	221	72.0	469	8	AD393939	Adl93939 Human G-c
39	221	72.0	470	8	ADN07695	Adn07695 Human mat
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41	221	72.0	496	4	AAG75509	Aag75509 Human col
42	215	70.0	457	1	AAP93628	Aap93628 Sequence
43	215	70.0	469	1	AAP70611	Aap70611 Sequence
44	215	70.0	469	8	ADQ18359	Adq18359 Human sof
45	214	69.7	54	6	ABP97131	Abp97131 Human mat

## ALIGNMENTS

## RESULT 1

ABP97132  
ID ABP97132 standard; peptide; 55 AA.

XX AC ABP97132;

XX AC (first entry)

DT 24-JUN-2003 (first entry)

DE Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;  
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;  
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;  
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;  
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;  
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;  
KW macular degeneration; diabetic retinopathy; cleavage region.

XX OS Homo sapiens.

XX PN WO2003018748-A2.

XX PD 06-MAR-2003.

XX PF 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Weart IF;

XX DR WPI; 2003-381408/36.

PT Anti-angiogenic composition comprising peptide inhibitor of matrix

PT metalloproteinase, useful for decreasing the expression of vascular

PT endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX CC The present invention describes an anti-angiogenic composition (I) for  
XX CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)  
XX CC comprises an effective amount of a peptide inhibitor of matrix  
XX CC metalloproteinase (MMP), where the peptide can inhibit the expression of  
XX CC VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,  
XX CC antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting  
 CC growth of tumours and diminishing tumours size. The tumour can be  
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.  
 CC (I) is also useful for treating injuries including wounds, surgical  
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful  
 CC for treating disorders characterised by excessive angiogenesis e.g.  
 CC macular degeneration and diabetic retinopathy. The present sequence  
 CC represents a human MMP cleavage region peptide, which is used in the  
 CC exemplification of the present invention  
 XX  
 XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 2  
 ABG76318  
 ID ABG76318 standard; protein; 55 AA.  
 XX  
 AC ABG76318;  
 XX  
 XX 10-MAY-2003 (first entry)  
 DT Human matrix metalloproteinase (MMP) peptide inhibitor #10.  
 DE  
 XX Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;  
 XX cleavage region; proenzyme form; cellular proliferation; fibroblast;  
 KW keratinocyte; healthy skin development; wound healing; scarring;  
 KW skin tone; wrinkle; anti-aging; vulnerary.  
 XX  
 OS Homo sapiens.

XX WO2003016520-A1.  
 FN  
 XX 27-FEB-2003.  
 PD  
 XX 15-AUG-2002; 2002WO-US026198.  
 PF  
 XX 16-AUG-2001; 2001US-0312726P.  
 PR  
 XX 21-DEC-2001; 2001US-00023376.  
 PR  
 XX 21-MAY-2002; 2002US-00153195.

XX (KIMB ) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix  
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for  
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases  
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have  
 CC peptide sequences related to the cleavage regions of the proenzyme forms  
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular  
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin  
 CC development, treating wounds, preventing scarring, improving skin tone,  
 CC reducing wrinkling and for simulating the development of smooth, healthy  
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing  
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3

ADQ17093  
 ID ADQ17093 standard; peptide; 55 AA.

XX  
 AC ADQ17093;

XX 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;  
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds  
 PT comprises peptide having sequence related to matrix metalloproteinase  
 PT proenzyme.

XX Example 1; SEQ ID NO 10; 60pp; English.

XX The present invention provides peptides and compositions containing such  
 CC peptides that are useful as agents to maintain healthy skin and to  
 CC promote the condition of the skin. The invention is useful for increasing  
 CC the amount of fibronectin in tissue. The invention is also useful for  
 CC encouraging the maintenance and development of healthy skin, preventing  
 CC and treating wrinkles and for treating wounds. The invention acts as  
 CC vulnerary and dermatological agents. The present sequence is human matrix  
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in  
 CC the exemplification of the invention.

XX Sequence 55 AA;

Query Match 100.0%; Score 307; DB 8; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55  
 DB 1 MORFFGLNVTGPNBETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4

AAG65357  
 ID AAG65357 standard; protein; 444 AA.

XX AAG65357;

XX 30-NOV-2001 (first entry)

DE Human MMP-8alt polypeptide.  
XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;  
KW anti-arthritis; cytostatic; anti-Parkinsonian; neuroprotective;  
KW neurotropic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; human; splice variant.  
XX Homo sapiens.  
OS  
XX US-973-H.  
PN  
XX 03-JUL-2001.  
PD  
XX 22-OCT-1998; 98US-00178002.  
PF  
XX 22-OCT-1998; 98US-00178002.  
PR  
XX (NOVS ) NOVARTIS AG.  
PA  
XX Hu S;  
PI  
XX WPI; 2001-431511/46.  
DR N-PSDB; AAH47515.  
XX  
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents  
PT and materials for discovering treatments and diagnostics to human  
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.  
PT  
XX  
PS Claim 11; Col 25-30; 25pp; English.  
XX  
XX The invention relates to human MMP-8alt polypeptide and polynucleotides.  
CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)  
CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant  
CC methodology. The polynucleotides and polypeptides may be used as research  
CC reagents and materials for the discovery of treatments and diagnostics to  
CC human disease, and as targets for identifying modulators. Inhibitors of  
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat  
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases  
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's  
CC disease and Huntington's disease. The present sequence represents the  
CC human MMP-8alt polypeptide  
XX  
SQ Sequence 444 AA;  
Query Match 100.0%; Score 307; DB 4; Length 444;  
Best Local Similarity 100.0%; Pred. No. 4.4e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTFCNPKWERTNLTIRNY 55  
DB 43 MQRFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTFCNPKWERTNLTIRNY 97  
RESULT 5  
AAB84610  
ID AAB84610 standard; protein; 467 AA.  
XX  
AC AAB84610;  
XX  
DT 05-SEP-2001 (first entry)  
XX  
DE Amino acid sequence of matrix metalloproteinase-8.  
XX  
KW Growth factor; protein inhibitor; protease; damaged tissue;  
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;  
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;  
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;  
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;  
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;  
KW vascular endothelial growth factor; urokinase plasminogen activator;  
KW dermal ulcer; wound.  
XX  
OS Homo sapiens.

XX WO200149309-A2.  
PN  
XX 12-JUL-2001.  
PD  
XX 21-DEC-2000; 2000WO-IB001935.  
PF  
XX 29-DEC-1999; 99GB-00030768.  
PR  
XX (PFIZ ) PFIZER LTD.  
PA (PFIZ ) PFIZER INC.  
XX  
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;  
PI WPI; 2001-418351/44.  
DR N-PSDB; AAH28225.  
XX  
XX Composition for the treatment of damaged tissue i.e. chronic wounds and  
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth  
PT factor.  
PT  
XX  
PS Disclosure; Page 555; 572pp; English.  
XX  
XX The specification describes a pharmaceutical composition, comprising a  
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent  
CC inhibits the action of at least one specific adverse protein, i.e. a  
CC protease, that is upregulated in a damaged tissue such as a wound  
CC environment. Growth factors which are included in the composition of the  
CC invention are platelet-derived growth factor (PDGF), fibroblast growth  
CC factor (FGF), connective tissue derived growth factor (CTGF),  
CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta  
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),  
CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),  
CC and chrysalin. Inhibitors which are included in the composition of the  
CC invention include inhibitors of urokinase-type plasminogen activator  
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for  
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.  
CC The present sequence represents a human MMP-8, and is used to produce the  
CC composition of the invention  
XX  
SQ Sequence 467 AA;  
Query Match 100.0%; Score 307; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MQRFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTFCNPKWERTNLTIRNY 55  
DB 66 MQRFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTFCNPKWERTNLTIRNY 120  
RESULT 6  
AAE10416  
ID AAE10416 standard; protein; 467 AA.  
XX  
AC AAE10416;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Human matrix metalloproteinase-8 (MMP-8) protein.  
XX  
KW Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;  
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20 /label= Signal\_peptide  
XX Protein 21..467 /label= Mature\_MMP\_8\_protein  
XX Domain 89..95 /label= Cysteine\_switch\_domain



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PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
XX
PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX
DR WPI; 2003-456290/43.
DR N-PSDB; ACD66741.
XX
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.
XX
XX Disclosure; Fig 15V-15W; 482pp; English.
XX
XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related protein of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 307; DB 6; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKPNNEETLDMKKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKPNNEETLDMKKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120
RESULT 9
ADQ10212
ID ADQ10212 standard; protein; 467 AA.
XX
AC ADQ10212;
XX
XX 09-SEP-2004 (first entry)
XX
XX Human polypeptide #75.
XX
XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;
KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;
KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;
KW arteriosclerosis; hypertension; bacterial infection; psoriasis;
KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;
KW goiter; infertility; endometriosis; muscular disorder.
XX
OS Homo sapiens.
XX
PN US2004121396-A1.
XX
PD 24-JUN-2004.
XX
PF 19-DEC-2003; 2003US-00741790.
XX
XX 14-JUN-1999; 99US-00333159.
XX 29-JUN-1999; 99US-00342364.
XX 10-SEP-1999; 99US-00393996.
XX 19-OCT-1999; 99US-00420707.
XX 07-JAN-2000; 2000US-00479249.
XX 27-APR-2000; 2000US-00559497.
XX 24-MAY-2000; 2000US-00578063.
XX 16-JUN-2000; 2000US-00596194.
XX 23-JUN-2000; 2000US-00602871.
XX 30-JUN-2000; 2000US-00608452.
XX 12-JAN-2001; 2001US-00759130.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
XX Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX
XX WPI; 2004-479675/45.
XX
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, goiter, infertility.
XX
XX Disclosure; SEQ ID NO 176; 483pp; English.
XX
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a
CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity,
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, malaria, goiter,
CC disease, AIDS, tuberculosis, viral infections, malaria, Parkinson's
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polypeptide of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 467 AA;
Query Match 100.0%; Score 307; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKPNNEETLDMKKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKPNNEETLDMKKKPCGVPDGGFMLTPGNPKWERTNLTIRNY 120
RESULT 10
ADL93947
ID ADL93947 standard; protein; 454 AA.
XX
AC ADL93947;
XX
XX 20-MAY-2004 (first entry)
XX

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PR 13-APR-2001; 2001US-0283678P.  
PR 13-APR-2001; 2001US-0283687P.  
PR 13-APR-2001; 2001US-0283710P.  
PR 17-APR-2001; 2001US-0284234P.  
PR 19-APR-2001; 2001US-0285323P.  
PR 20-APR-2001; 2001US-0285609P.  
PR 23-APR-2001; 2001US-0285748P.  
PR 23-APR-2001; 2001US-0285890P.  
PR 24-APR-2001; 2001US-0286068P.  
PR 27-APR-2001; 2001US-0287213P.  
PR 03-MAY-2001; 2001US-0288509P.  
PR 30-MAY-2001; 2001US-0294495P.  
PR 31-MAY-2001; 2001US-0294801P.  
PR 31-JUL-2001; 2001US-0309216P.  
PR 25-SEP-2001; 2001US-0324775P.  
PR 28-NOV-2001; 2001US-0333900P.  
PR 02-APR-2002; 2002US-00115479.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX  
XX WPI; 2003-067574/06.  
DR N-PSDB; ADE16001.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX  
XX Claim 1; SEQ ID NO 32; 320pp; English.  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC viricide, fungicide, cytostatic, and antilipemic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
XX Sequence 454 AA;  
SQ

Query Match 72.0%; Score 221; DB 7; Length 454;

Best Local Similarity 70.9%; Pred. NO. 2.9e-21;

Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVTKGKPDATLKVMPKQRCVDPVDAQFVLTGPNRWEOTHTLYRIENY 55

Db 50 MQRFFGLVTKGKPDATLKVMPKQRCVDPVDAQFVLTGPNRWEOTHTLYRIENY 104  
RESULT 12  
ADE16004  
XX ADE16004 standard; protein; 454 AA.  
XX AC ADE16004;  
XX DT 29-JAN-2004 (first entry)  
XX DE G-coupled protein receptor related polypeptide, SEQ ID NO 34.  
XX KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
KW viricide; fungicide; cytostatic; nootropic; neuroprotective;  
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;  
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
KW preventive medicine; pharmacogenomics; human.  
XX Homo sapiens.  
XX OS  
XX WO200283841-A2.  
XX FN  
XX PD 24-OCT-2002.  
XX  
XX 03-APR-2002; 2002WO-US010713.  
PF  
XX  
XX 03-APR-2001; 2001US-0281136P.  
PR  
XX 05-APR-2001; 2001US-0281863P.  
PR  
XX 10-APR-2001; 2001US-0281906P.  
PR  
XX 13-APR-2001; 2001US-0282934P.  
PR  
XX 13-APR-2001; 2001US-0283857P.  
PR  
XX 13-APR-2001; 2001US-0283678P.  
PR  
XX 13-APR-2001; 2001US-0283687P.  
PR  
XX 17-APR-2001; 2001US-0284234P.  
PR  
XX 19-APR-2001; 2001US-0285325P.  
PR  
XX 20-APR-2001; 2001US-0285609P.  
PR  
XX 23-APR-2001; 2001US-0285748P.  
PR  
XX 24-APR-2001; 2001US-0286068P.  
PR  
XX 27-APR-2001; 2001US-0287213P.  
PR  
XX 30-MAY-2001; 2001US-0288509P.  
PR  
XX 31-MAY-2001; 2001US-0294495P.  
PR  
XX 31-JUL-2001; 2001US-0309216P.  
PR  
XX 25-SEP-2001; 2001US-0324775P.  
PR  
XX 28-NOV-2001; 2001US-0333900P.  
PR  
XX 02-APR-2002; 2002US-00115479.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;  
XX  
XX WPI; 2003-067574/06.  
DR N-PSDB; ADE16003.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
PT Alzheimer's disease, infections.  
XX  
XX Claim 1; SEQ ID NO 34; 320pp; English.  
XX  
XX The invention relates to a novel isolated G-coupled protein receptor  
CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
CC defined sequences of 87-1780 amino acids, given in the specification;  
CC their mature forms; and possible variants. The novel polypeptides have  
CC the following activities: antidiabetic, anorectic, antibacterial,  
CC viricide, fungicide, cytostatic, and antilipemic. The G-coupled protein  
CC receptor related polypeptides are useful in a method of treating or  
CC preventing in a human, a pathology associated with the G-coupled protein  
CC receptor related polypeptides. The polypeptides are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The novel  
CC polypeptides are useful for treating, preventing or diagnosing diseases,  
CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
CC disorders, and various dyslipidemias, metabolic disturbances associated  
CC with obesity, metabolic X syndrome and wasting disorders associated with  
CC chronic diseases and various cancers. The nucleic acids and polypeptides  
CC may also be used as targets for the identification of small molecules  
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
CC substances for use in therapeutic or diagnostic methods. The nucleic  
CC acids are further used as hybridization probes, in chromosome mapping,  
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
CC represents one of the novel G-coupled protein receptor related  
CC polypeptides of the invention.  
XX  
XX Sequence 454 AA;  
SQ

CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOVX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.  
 XX  
 SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTGKPNBETLDMKKKPCGVPDSCGFMLTFCNPKWERTNLTIRNY 55  
 DB 50 MQEFFGLKVTGKPDATLTKVMQKPCGVPDVAQFVLTEGNPRWEQTHLYRNY 104

RESULT 13  
 ADE16008  
 ID ADE16008 standard; protein; 454 AA.  
 AC ADE16008;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE G-coupled protein receptor related polypeptide, SEQ ID No 38.  
 XX  
 KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;  
 KW antiparkinsonian; haemostatic; antilipaeamic; neuroprotective;  
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;  
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
 KW preventive medicine; pharmacogenomics; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283841-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 XX 03-APR-2002; 2002WO-US010713.

XX  
 PR 03-APR-2001; 2001US-0281136P.  
 PR 05-APR-2001; 2001US-0281863P.  
 PR 10-APR-2001; 2001US-0281906P.  
 PR 13-APR-2001; 2001US-0282934P.  
 PR 13-APR-2001; 2001US-0283657P.  
 PR 13-APR-2001; 2001US-0283678P.  
 PR 13-APR-2001; 2001US-0283687P.  
 PR 13-APR-2001; 2001US-0283710P.  
 PR 17-APR-2001; 2001US-0284234P.  
 PR 19-APR-2001; 2001US-0285325P.  
 PR 20-APR-2001; 2001US-0285609P.  
 PR 23-APR-2001; 2001US-0285748P.

PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.  
 PR 27-APR-2001; 2001US-0287213P.  
 PR 30-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 PR 02-APR-2002; 2002US-00115479.  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zertusen BD;  
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;  
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;  
 XX  
 DR WPI; 2003-067574/06.  
 DR N-PSDB; ADE16007.  
 XX  
 PT New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
 PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,  
 PT Alzheimer's disease, infections.  
 XX  
 PS Claim 1; SEQ ID NO 38; 320pp; English.

XX  
 CC The invention relates to a novel isolated G-coupled protein receptor  
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully  
 CC defined sequences of 87-1780 amino acids, given in the specification;  
 CC their mature forms; and possible variants. The novel polypeptides have  
 CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,  
 CC antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a  
 CC human disease, preferably a NOVX-associated disorder. The novel  
 CC polypeptides are useful for treating, preventing or diagnosing diseases,  
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,  
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,  
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, metabolic X syndrome and wasting disorders associated with  
 CC chronic diseases and various cancers. The nucleic acids and polypeptides  
 CC may also be used as targets for the identification of small molecules  
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell  
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene  
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX  
 CC substances for use in therapeutic or diagnostic methods. The nucleic  
 CC acids are further used as hybridization probes, in chromosome mapping,  
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence  
 CC represents one of the novel G-coupled protein receptor related  
 CC polypeptides of the invention.  
 XX  
 SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKKPCGVPDSCGFMLTFCNPKWERTNLTIRNY 55  
 DB 50 MQEFFGLKVTGKPDATLTKVMQKPCGVPDVAQFVLTEGNPRWEQTHLYRNY 104

RESULT 14  
 ADE16006  
 ID ADE16006 standard; protein; 454 AA.  
 XX



AC ADEL6006;  
 XX 29-JAN-2004 (first entry)  
 XX G-coupled protein receptor related polypeptide, SEQ ID NO 36.  
 DE  
 XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;  
 KW viricide; fungicide; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;  
 KW cell differentiation; cell proliferation; hematopoiesis;  
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;  
 KW preventive medicine; pharmacogenomics; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283841-A2.  
 PN  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 03-APR-2002; 2002WO-US010713.  
 XX  
 PR 03-APR-2001; 2001US-0281136P.  
 PR 05-APR-2001; 2001US-0281863P.  
 PR 05-APR-2001; 2001US-0281906P.  
 PR 10-APR-2001; 2001US-0282934P.  
 PR 13-APR-2001; 2001US-0283657P.  
 PR 13-APR-2001; 2001US-0283678P.  
 PR 13-APR-2001; 2001US-0283687P.  
 PR 13-APR-2001; 2001US-0283710P.  
 PR 17-APR-2001; 2001US-0284234P.  
 PR 19-APR-2001; 2001US-0285325P.  
 PR 20-APR-2001; 2001US-0285609P.  
 PR 23-APR-2001; 2001US-0285748P.  
 PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.  
 PR 27-APR-2001; 2001US-0287213P.  
 PR 30-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 PR 02-APR-2002; 2002US-00115479.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zethusen BD;  
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 PI Voss EZ, Vernet CAM, Maccougall JR, Rastelli L, Anderson DW;  
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shimkets RA, Taupier RJ, Edinger SR, Nazur A;  
 XX  
 XX WPI; 2003-067574/06.  
 DR N-PSDB; ADEL6005.  
 XX  
 XX New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.  
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,  
 PT Alzheimer's disease, infections.  
 XX  
 XX Claim 1; SEQ ID NO 36; 320pp; English.  
 PS  
 XX The invention relates to a novel isolated G-coupled protein receptor  
 CC related polypeptides. The novel polypeptide comprises any of the 22 fully  
 CC defined sequences of 87-1780 amino acids, given in the specification;  
 CC their mature forms; and possible variants. The novel polypeptides have  
 CC the following activities: antidiabetic, anorectic, antibacterial,  
 CC viricide, fungicide, cytostatic, and antilipemic. The G-coupled protein  
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein  
 CC receptor related polypeptides are useful in a method of treating or  
 CC preventing in a human, a pathology associated with the G-coupled protein  
 CC receptor related polypeptides. The polypeptides are useful in the  
 CC manufacture of a medicament for treating a syndrome associated with a

human disease, preferably a NOVX-associated disorder. The novel polypeptides are useful for treating, preventing or diagnosing diseases, such as metabolic disorders, diabetes, obesity, infectious diseases, anorexia, cancer-associated diseases, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic disorders, and various dyslipidemias, metabolic disturbances associated with obesity, metabolic X syndrome and wasting disorders associated with chronic diseases and various cancers. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. This sequence represents one of the novel G-coupled protein receptor related polypeptides of the invention.

Sequence 454 AA;  
 Query Match 72.0%; Score 221; DB 7; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYRINY 55  
 DB 50 MQEPPGLKVTGKPDATETLVKMKQPRCGVDPDAOFVLTEGNRWEQTHLTIRIENY 104  
 RESULT 15  
 ADL93945  
 ID ADL93945 standard; protein; 454 AA.  
 XX AC ADL93945;  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX Human G-coupled protein receptor-related protein #18.  
 DE  
 XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;  
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;  
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;  
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;  
 KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;  
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;  
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;  
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;  
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;  
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;  
 KW neurodegenerative disorder; receptor.  
 XX OS Homo sapiens.  
 XX  
 XX US2004006205-A1.  
 XX  
 XX 08-JAN-2004.  
 PD  
 XX  
 XX 02-APR-2002; 2002US-00115479.  
 PF  
 XX  
 XX 03-APR-2001; 2001US-0281136P.  
 PR 05-APR-2001; 2001US-0281863P.  
 PR 05-APR-2001; 2001US-0281906P.  
 PR 10-APR-2001; 2001US-0282934P.  
 PR 13-APR-2001; 2001US-0283657P.  
 PR 13-APR-2001; 2001US-0283678P.  
 PR 13-APR-2001; 2001US-0283697P.  
 PR 13-APR-2001; 2001US-0283710P.  
 PR 17-APR-2001; 2001US-0284234P.  
 PR 19-APR-2001; 2001US-0285325P.  
 PR 20-APR-2001; 2001US-0285609P.  
 PR 23-APR-2001; 2001US-0285748P.  
 PR 23-APR-2001; 2001US-0285890P.  
 PR 24-APR-2001; 2001US-0286068P.

27-APR-2001; 2001US-0287213P.  
 PR 03-MAY-2001; 2001US-0288509P.  
 PR 30-MAY-2001; 2001US-0294495P.  
 PR 31-MAY-2001; 2001US-0294801P.  
 PR 31-JUL-2001; 2001US-0309216P.  
 PR 25-SEP-2001; 2001US-0324775P.  
 PR 28-NOV-2001; 2001US-0333900P.  
 XX (LILL/) LI L.  
 PA (GERL/) GERLACH V.  
 PA (LIUX/) LIU X.  
 PA (MILL/) MILLER C E.  
 PA (SPYT/) SPYTEK K A.  
 PA (ZERH/) ZERHUSEN B D.  
 PA (PENA/) PENA C E A.  
 PA (SHEN/) SHENOY S G.  
 PA (ZHON/) ZHONG H.  
 PA (SMIT/) SMITHSON G.  
 PA (CASW/) CASMAN S J.  
 PA (BOLD/) BOLDOG F L.  
 PA (VOSS/) VOSS E Z.  
 PA (VERN/) VERNET C A.  
 PA (MACD/) MACDOUGALL J R.  
 PA (RAST/) RASTELLI L.  
 PA (ANDE/) ANDERSON D W.  
 PA (ZHON/) ZHONG M.  
 PA (MEZE/) MEZES P S.  
 PA (FURT/) FURTAK K.  
 PA (PATT/) PATTURAJAN M.  
 PA (BURG/) BURGESS C E.  
 PA (MALY/) MALYANKAR U M.  
 PA (SHIM/) SHIMKETS R A.  
 PA (TAUP/) TAUPIER R J.  
 PA (EDIN/) EDINGER S.  
 PA (MAZU/) MAZUR A.  
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;  
 PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;  
 PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;  
 PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;  
 PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;  
 XX WPI; 2004-224146/21.  
 DR N-PSDB; ADL93944.  
 XX New G-coupled protein-receptor related polypeptides, for preventing  
 PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,  
 PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,  
 PT scleroderma or obesity.  
 XX Claim 1; Page 68; 220pp; English.  
 PS The invention relates to isolated human G-coupled protein receptor-  
 CC related polypeptides and polynucleotides. The proteins are useful for  
 CC preventing, treating or ameliorating medical disorders by protein or gene  
 CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,  
 CC congenital heart defects, aortic stenosis, atrial septal defect,  
 CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,  
 CC subaortic stenosis, ventricular septal defect, valve diseases, tuberos  
 CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,  
 CC congenital adrenal hyperplasia, prostate cancer, neoplasm, hemophilia,  
 CC adenocarcinoma, lymphoma, uterine cancer, fertility, haemophilia,  
 CC hypercoagulation, idiopathic thrombocytopenic purpura,  
 CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,  
 CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They  
 CC are also useful as diagnostic or research tools. The present sequence  
 CC represents a human G-coupled protein receptor-related protein of the  
 CC invention.  
 XX Sequence 454 AA;  
 SQ Query Match 72.0%; Score 221; DB 8; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.9e-21;

Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 Qy 1 MQEFFGLNVTGKFNSEETLDMKKKPRCGVPSGGMFLTPGNPKWERTNLTYYRNY 55  
 Db 50 MQEFFGLKVTGKPDABETLKVKKQPRCGVPSGGMFLTPGNPKWERTNLTYYRNY 104  
 Search completed: October 13, 2004, 15:09:16  
 Job time : 105.359 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:02:10 ; Search time 26.0897 Seconds  
(without alignments)  
139.806 Million cell updates/sec

Title: US-10-032-376A-10  
Perfect score: 307  
Sequence: 1 MCRFFGLNVTGKPNKEETLDM.....LTPGNPKWERTNLTYYRINY 55

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 56318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	444	1 US-09-178-002-2	Sequence 2, Appli
2	307	100.0	456	3 US-08-704-711A-17	Sequence 17, Appl
3	307	100.0	466	3 US-09-521-220-17	Sequence 17, Appl
4	307	100.0	467	1 US-09-178-002-4	Sequence 4, Appli
5	307	100.0	467	3 US-09-391-104-24	Sequence 24, Appl
6	307	100.0	468	3 US-08-448-489-13	Sequence 13, Appl
7	221	72.0	469	3 US-08-704-711A-16	Sequence 16, Appl
8	221	72.0	469	3 US-08-448-489-12	Sequence 12, Appl
9	221	72.0	469	3 US-09-521-220-16	Sequence 16, Appl
10	221	72.0	469	3 US-09-391-104-23	Sequence 23, Appl
11	196	63.8	477	3 US-08-704-711A-20	Sequence 20, Appl
12	196	63.8	477	3 US-08-448-489-15	Sequence 15, Appl
13	196	63.8	477	3 US-08-281-313-1	Sequence 9, Appli
14	196	63.8	477	3 US-09-521-220-20	Sequence 20, Appl
15	196	63.8	477	3 US-09-391-104-21	Sequence 21, Appl
16	195	63.5	476	3 US-08-704-711A-21	Sequence 21, Appl
17	195	63.5	476	3 US-08-448-489-14	Sequence 14, Appl
18	195	63.5	476	3 US-09-521-220-21	Sequence 21, Appl
19	195	63.5	476	3 US-09-391-104-22	Sequence 22, Appl
20	188	61.2	471	3 US-09-391-104-25	Sequence 25, Appl
21	179	58.3	471	4 US-08-994-689C-1	Sequence 1, Appli
22	172	56.0	471	4 US-08-394-689C-21	Sequence 21, Appl
23	164	53.4	513	4 US-10-140-0002-192	Sequence 192, App
24	164	53.4	513	4 US-09-862-631-4	Sequence 4, Appli
25	160	52.1	264	3 US-09-009-156-6	Sequence 6, Appli
26	160	52.1	264	3 US-09-372-154-6	Sequence 6, Appli
27	160	52.1	267	3 US-08-448-489-18	Sequence 18, Appl

Sequence 27, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 26, Appli  
Sequence 30, Appli  
Sequence 4163, Ap  
Sequence 7, Appli  
Sequence 17, Appli  
Sequence 18, Appli  
Sequence 15, Appli  
Sequence 19, Appli  
Sequence 89, Appli  
Sequence 30, Appli  
Sequence 2, Appli  
Sequence 10, Appli  
Sequence 2, Appli  
Sequence 4639, Ap

ALIGNMENTS

RESULT 1  
US-09-178-002-2  
; Sequence 2, Application US/09178002  
; Patent No. H001973  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Shou-Ih  
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
; FILE REFERENCE: CGC 2048  
; CURRENT APPLICATION NUMBER: US/09/178,002  
; CURRENT FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 444  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;  
Best Local Similarity 100.0%; Pred. No. 5.2e-32;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCRFFGLNVTGKPNKEETLDMKKRCGVPDGGFMLTPGNPKWERTNLTYYRINY 55  
Db 43 MCRFFGLNVTGKPNKEETLDMKKRCGVPDGGFMLTPGNPKWERTNLTYYRINY 97

RESULT 2  
US-08-704-711A-17  
; Sequence 17, Application US/08704711A  
; Patent No. 6114159  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; APPLICANT: HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 3
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; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-521-220-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.5e-32; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu Shou-th
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CCC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 5.6e-32; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-16

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.le-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGPNKVERTNLTYYRIY 55
Db 67 MQEFGKLVTKGPDAAETLKVMPKPRCGVPDVAQFVLTEGPNRWEQHTLYRIENY 121

RESULT 8
US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.le-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPDGGFMLTPGPNKVERTNLTYYRIY 55
Db 67 MQEFGKLVTKGPDAAETLKVMPKPRCGVPDVAQFVLTEGPNRWEQHTLYRIENY 121

RESULT 9
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 639346
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd

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; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220.
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
;
; INFORMATION FOR SEQ ID NO: 16:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRINY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121

RESULT 10
US-09-391-104-23
; Sequence 23, Application US/093911104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLNTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRINY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121

RESULT 11
US-08-704-711A-20
; Sequence 20, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; INFORMATION FOR SEQ ID NO: 20:
US-08-704-711A-20

Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.8%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYRINY 55
Db 67 MQEFGKLVGTGPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLYRIENY 121
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RESULT 12  
US-08-448-489-15  
; Sequence 15, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-230P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-15

Query Match 63.8%; Score 196; DB 3; Length 477;  
Best Local Similarity 63.6%; Pred. No. 2.1e-17;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNNEETLDMKXPRGVDPSGFMFLTPGNPKWERTNLTIRINY 55  
Db 67 MQRFLGLEVTGKLDSTLEVMKPRGVDVGHFRTFGIPKWKRLTIRINY 121

RESULT 13  
US-08-281-313-1  
; Sequence 9, Application US/09368169  
; Patent No. 6284511  
; GENERAL INFORMATION:  
; APPLICANT: Tetsuya INAKA et al.  
; TITLE OF INVENTION: HEAT-STABLE PROLYNDOPEPTIDASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/368,169  
; FILING DATE: August 5, 1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/750,816  
; FILING DATE: January 8, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee Cheng  
; REGISTRATION NUMBER: 40,949  
; REFERENCES/DOCKET NUMBER: 99-0868/LC (WMC) 49  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-721-8200  
; TELEFAX: 202-721-8250  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acid residues  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; ORIGINAL SOURCE:  
; ORGANISM: Flavobacterium meningosepticum  
; ORGANISM: Met Lys Tyr Asn Lys Ser Val Ala Val Ala Ala Phe Ala Phe Ala Ala V  
; ORGANISM: 1  
; Sequence 1, Application US/08281313  
; Patent No. 6284513  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Qi-Zhuang  
; APPLICANT: Johnson, Linda L.  
; APPLICANT: Hupe, Donald J.  
; APPLICANT: Bakagi, Vijaykumar  
; TITLE OF INVENTION: Process for the Production of  
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Warner-Lambert Company  
; STREET: 2800 Plymouth Rd.  
; CITY: Ann Arbor  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,313  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012,705  
; FILING DATE: 03-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tinney, Francis J.  
; REGISTRATION NUMBER: 33,069  
; REFERENCE/DOCKET NUMBER: 4415-01-FJT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 313 996-7295  
; TELEFAX: 313 996-1553  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 477 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 100..273  
; OTHER INFORMATION: /note= "Mature stromelysin  
; OTHER INFORMATION: catalytic domain protein"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..17  
; OTHER INFORMATION: /note= "Signal peptide"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 18..99  
; OTHER INFORMATION: /note= "Propeptide"  
US-08-281-313-1

Query Match 63.8%; Score 196; DB 3; Length 477;  
Best Local Similarity 63.6%; Pred. No. 2.1e-17;  
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNNEETLDMKXPRGVDPSGFMFLTPGNPKWERTNLTIRINY 55  
Db 67 MQRFLGLEVTGKLDSTLEVMKPRGVDVGHFRTFGIPKWKRLTIRINY 121

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RESULT 14
US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horet
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.6%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKWKTKHLYRIVNY 121

RESULT 15
US-09-391-104-21
; Sequence 21, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
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; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073 US P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-21
Query Match 63.8%; Score 196; DB 3; Length 477;
Best Local Similarity 63.8%; Pred. No. 2.1e-17;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||
Db 67 MQKFLGLEVTGKLDSDTLEVMRKPRCGVDPDVGHFRTFPGIPKWKTKHLYRIVNY 121

Search completed: October 13, 2004, 15:17:05
Job time : 26.0897 secs
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RESULT 2  
US-10-153-185-10  
; Sequence 10, Application US/10153185  
; Publication No. US20030148959A1  
; GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds  
; FILE REFERENCE: 1443.034US1  
; CURRENT APPLICATION NUMBER: US/10/153,185  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-185-10

Query Match 100.0%; Score 307; DB 14; Length 55;  
Best Local Similarity 100.0%; Pred. No. 8.8e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
Db 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3  
US-10-219-561-10  
; Sequence 10, Application US/10219561  
; Publication No. US20030166567A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Stephen  
; APPLICANT: Malik, Sohail  
; APPLICANT: Villanueva, Julie M.  
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds  
; FILE REFERENCE: 1443.008US2  
; CURRENT APPLICATION NUMBER: US/10/219,561  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 10/032,376  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US 10/153,185  
; PRIOR FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: US 60/312,726  
; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-219-561-10

Query Match 100.0%; Score 307; DB 14; Length 55;  
Best Local Similarity 100.0%; Pred. No. 8.8e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
Db 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4  
US-10-032-376A-10  
; Sequence 10, Application US/10032376A  
; Publication No. US20040127420A1  
; GENERAL INFORMATION:  
; APPLICANT: Quirk, Steven  
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing  
; FILE REFERENCE: 1443.008US1  
; CURRENT APPLICATION NUMBER: US/10/032,376A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/312,726

; PRIOR FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-032-376A-10

Query Match 100.0%; Score 307; DB 16; Length 55;  
Best Local Similarity 100.0%; Pred. No. 8.8e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
Db 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 5  
US-10-335-207-10  
; Sequence 10, Application US/10335207  
; Publication No. US20040127421A1  
; GENERAL INFORMATION:  
; APPLICANT: Malik, Sohail  
; APPLICANT: Quirk, Stephen  
; TITLE OF INVENTION: Method to Increase Fibrinectin  
; FILE REFERENCE: 1443.047US1  
; CURRENT APPLICATION NUMBER: US/10/335,207  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-335-207-10

Query Match 100.0%; Score 307; DB 16; Length 55;  
Best Local Similarity 100.0%; Pred. No. 8.8e-33;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
Db 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 6  
US-09-391-104-24  
; Sequence 24, Application US/09391104  
; Publication No. US20020031817A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Falduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
; TITLE OF INVENTION: OF USING SAME  
; FILE REFERENCE: 6073 US. P1  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; PRIOR FILING DATE: 1997-03-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-24

Query Match 100.0%; Score 307; DB 9; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.1e-31;

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Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 7
US-09-801-196-20
; Sequence 20, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; TITLE OF INVENTION: EXPRESSED IN SKIN CELLS
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801,196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-20

Query Match 100.0%; Score 307; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 8
US-09-759-130B-176
; Sequence 176, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MP100-5350NIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
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; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-176

Query Match 100.0%; Score 307; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 9
US-10-131-985-31
; Sequence 31, Application US/10131985
; Publication No. US2003019940A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-31

Query Match 100.0%; Score 307; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 10
US-10-741-790-176
; Sequence 176, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
```

APPLICANT: Myers, Paul S  
APPLICANT: Leiby, Kevin R  
APPLICANT: Wrighton, Nicolas  
APPLICANT: Goodearl, Andrew  
APPLICANT: Holtzman, Douglas A  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES  
FILE REFERENCE: MPI00-5350NMIM  
CURRENT APPLICATION NUMBER: US/10/741,790  
CURRENT FILING DATE: 2003-12-19  
PRIOR APPLICATION NUMBER: US 09/479,249  
PRIOR FILING DATE: 2000-01-07  
PRIOR APPLICATION NUMBER: US 09/559,497  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 09/578,063  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/333,159  
PRIOR FILING DATE: 1999-06-14  
PRIOR APPLICATION NUMBER: US 09/596,194  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/342,364  
PRIOR FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: US 09/608,452  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/393,996  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 09/602,871  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: US 09/420,707  
PRIOR FILING DATE: 1999-10-19  
NUMBER OF SEQ ID NOS: 460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.1e-31;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MQRFFGLVNTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYIRNY 55  
Db 66 MQRFFGLVNTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYIRNY 120

RESULT 11  
US-10-115-479-32  
Sequence 32, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna

APPLICANT: Patturajan, Meera  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Malyanker, Uriel M.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Mazur, Ann  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-322 B (Cura 622 PI)  
CURRENT APPLICATION NUMBER: US/10/115,479  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 60/281,136  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 60/281,863  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/281,906  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/282,934  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: 60/283,657  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,678  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,687  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/283,710  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 60/284,234  
PRIOR FILING DATE: 2001-04-17  
PRIOR APPLICATION NUMBER: 60/285,325  
PRIOR FILING DATE: 2001-04-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 198  
SEQ ID NO 32  
LENGTH: 454  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-115-479-32

Query Match 72.0%; Score 221; DB 15; Length 454;  
Best Local Similarity 70.9%; Pred. No. 2.3e-20;  
Matches 33; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
Qy 1 MQRFFGLVNTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYIRNY 55  
Db 50 MQRFFGLVNTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTYYIRNY 104

RESULT 12  
US-10-115-479-34  
Sequence 34, Application US/10115479  
Publication No. US20040006205A1  
GENERAL INFORMATION:  
APPLICANT: Li, Li  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Zhong, Haihong  
APPLICANT: Smithson, Glendda  
APPLICANT: Casman, Stacie J.  
APPLICANT: Boldog, Ferenc L.;  
APPLICANT: Voss, Edward  
APPLICANT: Vernet, Corine  
APPLICANT: MacDougall, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Anderson, David W.  
APPLICANT: Zhong, Mei  
APPLICANT: Mezes, Peter S.  
APPLICANT: Furtak, Katarzyna

```
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 34
/ LENGTH: 454
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-115-479-34
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Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.3e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
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OY 1 MQFFGLNVTGKNEETDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLTIRNY 104
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## RESULT 13

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US-10-115-479-36
/ Sequence 36, Application US/10115479
/ Publication No. US20040006205A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Li, Li
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Spyttek, Kimberly A.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Boldog, Ferenc L.;
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
```

```
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyanker, Uriel M.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Mazur, Ann
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-322 B (Cura 622 PT)
/ CURRENT APPLICATION NUMBER: US/10/115,479
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 60/281,136
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 60/281,863
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/281,906
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/282,934
/ PRIOR FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: 60/283,657
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,678
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,687
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/283,710
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,234
/ PRIOR FILING DATE: 2001-04-17
/ PRIOR APPLICATION NUMBER: 60/285,325
/ PRIOR FILING DATE: 2001-04-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 198
/ SEQ ID NO 36
/ LENGTH: 454
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-115-479-36
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Query Match 72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.3e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
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OY 1 MQFFGLNVTGKNEETDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRNY 55
Db 50 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLTIRNY 104
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## RESULT 14

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US-10-115-479-38
/ Sequence 38, Application US/10115479
/ Publication No. US20040006205A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Li, Li
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Spyttek, Kimberly A.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Boldog, Ferenc L.;
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
```

; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Burgess, Catherine E.  
 ; APPLICANT: Malyanker, Uriel M.  
 ; APPLICANT: Shinkets, Richard A.  
 ; APPLICANT: Taupier, Raymond J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Mazur, Ann  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)  
 ; CURRENT APPLICATION NUMBER: US/10/115,479  
 ; CURRENT FILING DATE: 2002-11-18  
 ; PRIOR APPLICATION NUMBER: 60/281,136  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/281,863  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/281,906  
 ; PRIOR FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/282,934  
 ; PRIOR FILING DATE: 2001-04-10  
 ; PRIOR APPLICATION NUMBER: 60/283,657  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,678  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,687  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/283,710  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,234  
 ; PRIOR FILING DATE: 2001-04-17  
 ; PRIOR APPLICATION NUMBER: 60/285,325  
 ; PRIOR FILING DATE: 2001-04-19  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SEQ ID NO 38  
 ; LENGTH: 454  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-115-479-38

Query Match 72.0%; Score 221; DB 15; Length 454;  
 Best Local Similarity 70.9%; Pred. No. 2.3e-20;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPNETLDMKKKPRGCVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
 Db 50 MQEFFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGPRWEQTHLTIRIENY 104

RESULT 15  
 US-09-391-104-23  
 ; Sequence 23, Application US/093911104  
 ; Publication No. US20020031817A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbott Laboratories  
 ; APPLICANT: Falduto, Michael T.  
 ; APPLICANT: Magnuson, Scott R.  
 ; APPLICANT: Morgan, Douglas W.  
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,  
 ; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
 ; TITLE OF INVENTION: OF USING SAME  
 ; FILE REFERENCE: 6073.US.P1  
 ; CURRENT APPLICATION NUMBER: US/09/391,104  
 ; CURRENT FILING DATE: 1999-09-07  
 ; PRIOR APPLICATION NUMBER: US 08/814,394  
 ; PRIOR FILING DATE: 1997-03-11  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 469  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-391-104-23

Query Match 72.0%; Score 221; DB 9; Length 469;  
 Best Local Similarity 70.9%; Pred. No. 2.4e-20;  
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 Qy 1 MQRFFGLNVTGKPNETLDMKKKPRGCVDPDSGGFMLTPGNPKWERTNLTIRNY 55  
 Db 67 MQEFFFGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGPRWEQTHLTIRIENY 121

Search completed: October 13, 2004, 15:35:40  
 Job time : 78.2692 secs

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OM protein - protein search, using sw model

Run on: October 13, 2004, 15:01:19 ; Search time 20.8013 Seconds  
(without alignments)  
254.404 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKPNETLDM.....LTPGNPKWERTNLTLYRNY 55

Scoring table: BLOSUM62

Gapop'10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collage
2	233	75.9	468	1 KCRBI	interstitial colla
3	231	75.2	469	1 KCPGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCB0I	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 JC6505	stromelysin 2 (EC
10	193	62.9	477	1 KCMSS1	stromelysin 1 (EC
11	192	62.5	478	1 KCRBS1	stromelysin 1 (EC
12	190	61.9	476	1 KCRTS2	stromelysin 2 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KCPTIH	stromelysin 1 (EC
17	183	59.6	483	2 JC5743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	metalloelastase HM
21	160	52.1	663	1 S46492	gelatinase A (EC 3
22	155	50.5	662	2 S70365	gelatinase A (EC 3
23	153	49.8	660	1 A28153	gelatinase A (EC 3
24	153	49.8	662	2 A42496	gelatinase A (EC 3
25	153	49.8	662	2 A34780	gelatinase A (EC 3
26	139.5	45.4	669	2 I38029	matrix metalloprot
27	138	45.0	662	2 A42401	macrophage elastat
28	134.5	43.8	582	2 I38028	matrix metalloprot
29	134.5	43.8	582	2 I84471	matrix metalloprot

#### ALIGNMENTS

##### RESULT 1

KCHUN

neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human

N:Alternate names: matrix metalloproteinase 8

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C/Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32527; S6

R/Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stev

J. Biol. Chem. 265, 11421-11424, 1990

A/Title: Human neutrophil collagenase. A distinct gene product with homology to other m

A/Reference number: A37073; MUID:90307647; PMID:2164002

A/Accession: A37073

A/Molecule type: mRNA

A/Residues: 1-467 <HAS>

A/Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G18061

R/Devavajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.

Blood 77, 2731-2738, 1991

A/Title: Structure and expression of the cDNA encoding human neutrophil collagenase.

A/Reference number: A61175; MUID:91255696; PMID:1646048

A/Accession: A61175

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-31,'I',33-86,'E',88-467 <DEV>

A/Accession: B61175

A/Molecule type: protein

A/Residues: 263-264,'X',266-270,'X',272-273,'X',275,'X',277 <DE2>

R/Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.;

Biochemistry 29, 10628-10634, 1990

A/Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison wit

A/Reference number: A36230; MUID:91104978; PMID:2176876

A/Accession: A36230

A/Molecule type: protein

A/Residues: 'X',86-87,'X',89-90,'X',92-97,'X',99-111,'X',113-120 <MAL>

R/Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 189, 295-300, 1990

A/Title: Characterization and activation of procollagenase from human polymorphonuclear

A/Reference number: S09680; MUID:90249372; PMID:2159879

A/Accession: S09680

A/Molecule type: protein

A/Residues: 21-31,'I',33-39,'I',41-47,'V',49-53,'I',55-72,'G',74-86,'E',88-111,'X',113-

A/Note: 67-Lys was also found

R/Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Biol. Chem. Hoppe-Seyler 371, 733, 1990

A/Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase

A/Reference number: S11026; MUID:91000455; PMID:2169766

A/Accession: S11026

A/Note: original publication was Biol. Chem. Hoppe-Seyler 371(Suppl.), 295-304, 1990

A/Molecule type: protein

A/Residues: 21-31,'I',33-53,'I',55-72,'G',74-111,'X',113-140;183-203,'X',205-209;248-26

A/Note: 87-Glu was also found

R/Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 202, 1223-1230, 1991

[illegible]





tion peptide by other proteinases.

C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.

C;Genetics:

A;Gene: GDB:MMP1; CLG

A;Cross-references: GDB:119783; OMIM:120353

A;Map position: 11q22.2-11q22.3

C;Function:

A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and other proteins; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-469/Product: procollagenase #status experimental <PRO>

F;20-99/Domain: activation peptide #status experimental <ACT>

F;60-261/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-466/Product: interstitial collagenase #status experimental <MAT>

F;272-466/Domain: hemopexin repeat homology <PXN>

F;92-218, 222, 228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;120-143/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218, 222, 228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental

F;278-466/Disulfide bonds: #status experimental

Query Match 72.0%; Score 221; DB 1; Length 469;

Best Local Similarity 70.9%; Pred. No. 5.2e-20; Mismatches 9; Indels 0; Gaps 0;

Matches 39; Conservative 7;

QY 1 MQRFFGLNVTGKNEETLDMKKKPGVDSGGFMTLPGNPKWERTNLTIRNY 55

Db 67 MQEFGKLVTKGPDATLTKMKQPCGVPDVAQFVLTEGPNRWETHLTIRNY 121

RESULT 5

KCSOI

Interstitial collagenase (EC 3.4.24.7) precursor - bovine

N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase

C;Species: Bos primigenius taurus (Cattle)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004

C;Accession: S14654; S20336; S14655

C;Tamara, M.; Shimokawa, H.; Sasaki, S.

submitted to the EMBL Data Library, March 1991

A;Reference number: S14654

A;Accession: S14654

A;Molecule type: mRNA

A;Residues: 1-469 <MAT>

A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:9259; PIDN:CAA41210.1; PID:9260

R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.

Arch. Biochem. Biophys. 293, 370-376, 1992

A;Title: Purification and characterization of bovine interstitial collagenase and tissue

submitted to the EMBL Data Library, March 1991

A;Reference number: S20336; MUID:92161820; PMID:1311165

A;Accession: S20336

A;Molecule type: protein

A;Residues: 19-21, 'FP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125

C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Pep site in the

activation peptide by other proteinases.

C;Function: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.

A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and other proteins; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-469/Product: procollagenase #status predicted <PRO>

F;19-99/Domain: activation peptide #status predicted <ACT>

F;60-261/Domain: matrix metalloproteinase homology <MMP>

F;90-97/Region: autoinhibitory

F;100-466/Product: interstitial collagenase #status predicted <MAT>

F;272-466/Domain: hemopexin repeat homology <PXN>

F;92-218, 222, 228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;120-143/Binding site: carboxylate (Asn) (covalent) #status predicted

F;218, 222, 228/Binding site: zinc, catalytic (His) (active) #status predicted

F;219/Active site: Glu #status predicted

F;278-466/Disulfide bonds: #status predicted

Query Match 71.0%; Score 218; DB 1; Length 469;

Best Local Similarity 70.9%; Pred. No. 1.3e-19;

Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKKPGVDSGGFMTLPGNPKWERTNLTIRNY 55

Db 67 MQEFGKLVTKGPDATLTKMKQPCGVPDVAQFVLTEGPNRWETHLTIRNY 121

RESULT 6

151267

collagenase (EC 3.4.24.7) - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C;Accession: I51267

R;Oofusa, K.; Yomori, S.; Yoshizato, K.

Int. J. Dev. Biol. 38, 345-350, 1994

A;Title: Regionally and hormonally regulated expression of genes of collagen and collage

A;Reference number: I51267; MUID:95071832; PMID:7981043

A;Accession: I51267

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-384 <COF>

A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:913070; PIDN:AAB32661.1; PID:913071

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase

C;Keywords: hydrolase; metalloproteinase; zinc; zymogen

F;53-231/Domain: matrix metalloproteinase homology <MMP>

F;236-381/Domain: hemopexin repeat homology <PXN>

F;81, 189, 193, 199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted

F;189, 193, 199/Binding site: zinc, catalytic (His) (active) #status predicted

F;190/Active site: Glu #status predicted

Query Match 65.6%; Score 201.5; DB 2; Length 384;

Best Local Similarity 65.5%; Pred. No. 1.2e-17;

Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MQRFFGLNVTGKNEETLDMKKKPGVDSGGFMTLPGNPKWERTNLTIRNY 55

Db 57 LKQFGLKVTGKPDATLTKMKQPCGVPDVAQFVLTEGPNRWETHLTIRNY 110

RESULT 7

KCHUS1

stromelysin 1 (EC 3.4.24.17) precursor [validated] - human

N;Alternate names: angiotensin-converting enzyme; collagenase activating protein; matrix

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004

C;Accession: A28156; C29157; A28399; A60964; S15427

R;Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.

J. Biol. Chem. 263, 6742-6745, 1988

A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi

A;Reference number: A28156; MUID:88198243; PMID:3360803

A;Accession: A28156

A;Molecule type: mRNA

A;Residues: 1-44, 'E', '46-477 <SAU>

A;Cross-references: UNIPROT:P08254; GB:J03209; NID:9188618; PIDN:AAA36321.1; PID:9188619

R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysi

A;Reference number: A90336; MUID:87156645; PMID:3030290

A;Accession: C29157

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-477 <WHI>

A;Cross-references: EMBL:X05232; NID:936632; PIDN:CAA28859.1; PID:936633

R;Wilhelm, S.M.; Collier, I.E.; Kronberger, A.; Eisen, A.Z.; Warner, B.L.; Grant, G.A.;

Proc. Natl. Acad. Sci. U.S.A. 84, 6725-6729, 1987

A;Title: Human skin fibroblast stromelysin: structure, glycosylation, substrate specific

A;Reference number: A28399; MUID:88016164; PMID:3477804

A;Accession: A28399

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

```

Query Match      63.5%; SCORE 195; DB 1; Length 476;
Best Local Similarity 63.6%; Pred. No. 1a-16;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps
Gaps
QY      1  MORFGLNVTGKPNNEETLDMKKPRCGVDSGFMLTGPNPKWERTNLTYYRNY 55
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db       66  MOKFLGLEVTGKLDITLEVMRPRCGVDFVGHFSFGMPKWRKTLTYRVNY 120
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 9
JC8505
stromelysin 2 (EC 3.4.24.22) precursor - mouse
N;Alternate names: matrix metalloproteinase 10
C;Species: Mus musculus (house mouse)
C;Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2001
C;Accession: J06505
R;Madtener, M.; Werner, S.
Gene 202, 75-81, 1997

```





A:Gene: GDB:MPI3; CLG3  
A:Cross-references: GDB:373966; OMIM:600108  
A:Map position: 11q22.2-11q22.3  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; zinc; zymogen  
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F:64-267/Domain: matrix metalloproteinase homology <MMP>  
F:278-471/Domain: hemopexin repeat homology <PXN>  
F:96-222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted  
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;  
Best Local Similarity 63.6%; Pred. No. 7.9e-16;  
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 MRRFGLNVTGKNEETLDMKKPCGVPDSCGFMLTGCPNPKWERTNLTIRNY 55  
Db 71 MOSFFGLEVTGKLDONTLDVMKKPCGVPDVGGEYNVFPRTLKWSKQNLTYRINY 125

Search completed: October 13, 2004, 15:15:45  
Job time : 20.8013 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 15:00:44 ; Search time 112.821 Seconds  
(without alignments)  
280.495 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MRFPGNLNVCKPNEETLDM.....LTPGNPKWERTNLTYLRNY 55

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 MM08_HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01_RABIT	P13943 cryptolagus
3	231	75.2	469	1 MM01_PIG	P21692 sus scrofa
4	223	72.6	466	1 MM08_RAT	O88766 rattus norv
5	222	72.3	469	1 MM01_HORSE	Q9X825 equus cabal
6	221	72.0	469	1 MM01_HUMAN	P03956 homo sapien
7	221	72.0	469	2 AAP35520	AAP35520 homo sapi
8	218	71.0	469	1 MM01_BOVIN	P28053 bos taurus
9	201.5	65.6	384	1 MM01_RANCA	Q11133 rana catesb
10	198	64.5	465	2 Q8C209	Q8C209 mus muscu
11	198	64.5	465	2 Q8C230	Q8C230 mus muscu
12	198	64.5	465	2 AAH42742	AAH42742 mus muscu
13	198	64.5	465	2 BAC40805	BAC40805 mus muscu
14	198	64.5	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
15	198	64.5	478	2 AAO63580	AAO63580 canis fam
16	196	63.8	469	1 MM13_XENLA	Q10835 xenopus lae
17	196	63.8	472	2 Q93342	Q93342 gallus gall
18	196	63.8	472	2 Q10833	Q10833 xenopus lae
19	196	63.8	477	1 MM03_HUMAN	P09254 homo sapien
20	196	63.8	477	2 AAH69676	AAH69676 homo sapi
21	196	63.8	477	2 AAH69716	AAH69716 homo sapi
22	195	63.5	476	1 MM10_HUMAN	P09238 homo sapien
23	195	63.5	476	2 AAP36110	AAP36110 homo sapi
24	194	63.2	145	2 Q9N283	Q9N283 bos taurus
25	194	63.2	452	2 Q9NT82	Q9NT82 canis fami
26	193	62.9	476	1 MM10_MOUSE	O55123 mus muscu
27	193	62.9	477	1 MM03_MOUSE	P28862 mus muscu
28	193	62.9	479	2 Q922W6	Q922W6 mus muscu
29	192	62.5	478	1 MM03_RABIT	P28863 cryptolagus
30	190	61.9	465	1 MM08_MOUSE	O70138 mus muscu
31	190	61.9	476	1 MM10_RAT	P07152 rattus norv

32 189 61.6 466 1 MM13\_RAT  
33 189 61.6 472 1 MM13\_MOUSE  
34 188 61.2 383 2 Q7Z5M0  
35 188 61.2 393 2 Q8M118  
36 188 61.2 471 1 MM13\_HUMAN  
37 188 61.2 471 2 Q6NWN6  
38 188 61.2 471 2 AAH67522  
39 188 61.2 471 2 AAH67523  
40 188 61.2 475 1 MM03\_RAT  
41 188 61.2 489 2 Q7Z5M1  
42 187 60.9 472 1 MM13\_HORSE  
43 185 60.3 139 2 Q9GM68  
44 185 60.3 471 1 MM13\_BOVIN  
45 184 59.9 259 2 Q6DF35

P23097 rattus norv  
P33435 mus musculu  
Q7Z5M0 homo sapien  
Q8M118 felis silve  
P45452 homo sapien  
Q6NWN6 homo sapien  
AAH67522 homo sapi  
AAH67523 homo sapi  
P03957 rattus norv  
Q7Z5M1 homo sapien  
O18927 equus cabal  
Q9GM68 sus scrofa  
O76656 bos taurus  
Q6DF35 xenopus tro

#### ALIGNMENTS

RESULT 1  
MM08\_HUMAN STANDARD; PRT; 467 AA.  
ID P22894;  
AC P22894;  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DE 01-AUG-1991 (Rel. 19, Last sequence update)  
DE 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix  
DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).  
GN Name=MMP8; Synonyms=CLG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90307647; PubMed=2164002;  
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,  
RA Spinella D.G., Stevens R.M., Mainardi C.L.;  
RT "Human neutrophil collagenase. A distinct gene product with homology  
RT to other matrix metalloproteinases.";  
RL J. Biol. Chem. 265:11421-11424(1990).  
[2]  
SEQUENCE OF 21-140.  
RC TISSUE=Neutrophils;  
RX MEDLINE=90249372; PubMed=2159879;  
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RT "Characterization and activation of procollagenase from human  
RT polymorphonuclear leucocytes. N-terminal sequence determination of the  
RT proenzyme and various proteolytically activated forms.";  
RL Eur. J. Biochem. 189:295-300(1990).  
[3]  
SEQUENCE OF 21-103.  
RC TISSUE=Neutrophils;  
RX MEDLINE=92111500; PubMed=1662606;  
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;  
RT "Mercurial activation of human polymorphonuclear leucocyte  
RT procollagenase.";  
RL Eur. J. Biochem. 202:1223-1230(1991).  
[4]  
SEQUENCE OF 85-120, AND CHARACTERIZATION.  
RC TISSUE=Neutrophils;  
RX MEDLINE=91104978; PubMed=2176876;  
RA Mallya S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,  
RA Birkedal-Hansen H., van Wart H.E.;  
RT "Characterization of 58-kilodalton human neutrophil collagenase:  
RT comparison with human fibroblast collagenase.";  
RL Biochemistry 29:10628-10634(1990).  
[5]  
PARTIAL SEQUENCE.  
RC MEDLINE=90380298; PubMed=2169256;  
RX Knaeuper V., Kraemer S., Reinke H., Tschesche H.;  
RA "Partial amino acid sequence of human PMN leukocyte procollagenase.";

RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).  
RN [6]  
RP ERRATUM.  
RX MEDLINE=91000455; PubMed=2169766;  
RA Knauper V., Kraemer S., Reinke H., Tschesche H.;  
RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).  
RN [7]  
RP CYS-STEIN-SWITCH MECHANISM.  
RX TISSUE-Neutrophils;  
RA MEDLINE=93050220; PubMed=1330697;  
RL Blaser J., Triebel S., Reinke H., Tschesche H.;  
RN "Formation of a covalent Hg-Cys-bond during mercurial activation of  
PMNL procollagenase gives evidence of a cysteine-switch mechanism.";  
RL FEBS Lett. 313:59-61(1992).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.  
RX MEDLINE=94185631; PubMed=8137810;  
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;  
RN "The X-ray crystal structure of the catalytic domain of human  
neutrophil collagenase inhibited by a substrate analogue reveals the  
essentials for catalysis and specificity.";  
RL EMBO J. 13:1263-1269(1994).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.  
RX MEDLINE=94139330; PubMed=8307185;  
RA Reinemer P., Grams F., Huber R., Klein T., Schnierer S., Piper M.,  
RN Tschesche H., Bode W.;  
RT "Structural implications for the role of the N terminus in the  
RT 'superactivation' of collagenases. A crystallographic study.";  
RL FEBS Lett. 338:227-233(1994).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.  
RX MEDLINE=95384762; PubMed=7656015;  
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,  
RN Oronfleh M.W., Banks T.M., Rubin B.;  
RT "Structure of human neutrophil collagenase reveals large S1'  
RT specificity pocket.";  
RL Nat. Struct. Biol. 1:119-123(1994).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.  
RX MEDLINE=97390108; PubMed=9249047;  
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,  
RN Bode W., Gomis-Ruth F.-X.;  
RT "1.8-A crystal structure of the catalytic domain of human neutrophil  
RT collagenase (matrix metalloproteinase-8) complexed with a  
RT peptidomimetic hydroxamate primed-side inhibitor with a distinct  
RT selectivity profile.";  
RL Eur. J. Biochem. 247:356-363(1997).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.  
RX MEDLINE=98318039; PubMed=9655333;  
RA Brandstetter H., Engh R.A., von Roeder E.G., Moroder L., Huber R.,  
RN Bode W., Grams F.;  
RT "Structure of malonic acid-based inhibitors bound to human neutrophil  
RT collagenase. A new binding mode explains apparently anomalous data.";  
RL Protein Sci. 7:1303-1309(1998).  
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.  
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the  
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves  
CC type III collagen more slowly than type I.  
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.  
CC -!- ENZYME REGULATION: Cannot be activated without removal of the  
CC activation peptide.  
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.  
CC -!- TISSUE SPECIFICITY: Neutrophils.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J05556; AAA88021.1; -.  
DR PIR: A37073; KCHUN.  
DR PDB: 1A85; X-ray; A=105-262.  
DR PDB: 1A86; X-ray; A=105-262.  
DR PDB: 1B23; X-ray; A=99-263.  
DR PDB: 1I73; X-ray; A=100-262.  
DR PDB: 1I76; X-ray; A=100-262.  
DR PDB: 1JAN; X-ray; A=99-262.  
DR PDB: 1JAO; X-ray; A=100-262.  
DR PDB: 1JAP; X-ray; A=100-262.  
DR PDB: 1JQA; X-ray; A=100-262.  
DR PDB: 1JH1; X-ray; A=105-262.  
DR PDB: 1JH9; X-ray; A=100-262.  
DR PDB: 1KBC; X-ray; A=99-262.  
DR PDB: 1MNB; X-ray; A=100-262.  
DR PDB: 1MNC; X-ray; A=100-262.  
DR MEROPS: M10.002; -.  
DR Genew; HGNC:7175; MMP8.  
DR MIM: 120355; -.  
DR GO: GO:0005615; C:extracellular space; TAS.  
DR GO: GO:0008130; F:neutrophil collagenase activity; TAS.  
DR GO: GO:0008270; F:zinc ion binding; TAS.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; TAS.  
DR InterPro: IPR000585; Hemopexin.  
DR InterPro: IPR001818; Pept\_M10A\_M12B.  
DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro: IPR009070; PGSD\_like.  
DR Pfam: PF00445; Hemopexin; 4.  
DR Pfam: PF00413; Peptidase M10; 1.  
DR Pfam: PF03933; Peptidase M10\_N; 1.  
DR PRINTS: PRO0138; MATRINX.  
DR PROSITE: PS00546; CYSTEINE SWITCH; 1.  
DR PROSITE: PS00024; HEMOPEXIN; 1.  
DR PROSITE: PS00142; ZINC PROTEASE; 1.  
DR 3D-structure; Calcium-binding; Collagen degradation;  
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;  
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.  
FT SIGNAL 1 20 Activation peptide.  
FT PROPEP 21 100 Neutrophil collagenase.  
FT CHAIN 101 467 Hemopexin-like.  
FT DOMAIN 276 467 Cysteine switch.  
FT SITE 31 31  
FT METAL 157 157 Calcium 1.  
FT METAL 167 167 Zinc 1.  
FT METAL 169 169 Zinc 1.  
FT METAL 174 174 Calcium 2.  
FT METAL 175 175 Calcium 2 (via carbonyl oxygen).  
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).  
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).  
FT METAL 182 182 Zinc 1.  
FT METAL 189 189 Calcium 1.  
FT METAL 191 191 Calcium 1.  
FT METAL 193 193 Zinc 1.  
FT METAL 195 195 Calcium 2.  
FT METAL 197 197 Zinc 2 (catalytic).  
FT METAL 200 200 Zinc 2 (catalytic).  
FT METAL 217 217 Zinc 2 (catalytic).  
FT ACT\_SITE 218 218 Calcium 3 (via carbonyl oxygen) (By  
FT METAL 221 221 similarity).  
FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By  
FT METAL 286 286 similarity).  
FT METAL 378 378 Calcium 3 (via carbonyl oxygen) (By  
FT METAL 425 425 similarity).  
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Probable).  
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Probable).  
FT CARBOHYD 112 112 N-linked (GlcNAc...)  
FT CARBOHYD 204 204 N-linked (GlcNAc...)  
FT



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FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 279 464 Probable.

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.1e-26; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTFCNPKWERTNLTIRNY 55
    |||||
Db 66 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTFCNPKWERTNLTIRNY 120

RESULT 2
MM01_RABIT STANDARD; PRT; 468 AA.
ID MM01_RABIT
AC P13943;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name=MMP1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Synovial cell;
RX MEDLINE=88077876; PubMed=2825772;
RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
RT "A gene for rabbit synovial cell collagenase: member of a family of
RT metalloproteinases that degrade the connective tissue matrix.";
RL Biochemistry 26:6156-6165 (1987).
RN [2]
RP SEQUENCE OF 449-468 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=87029174; PubMed=3021384;
RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
RA Brinckerhoff C.E.;
RT "Homology between exon-containing portions of rabbit genomic clones
RT for synovial cell collagenase and human foreskin and synovial cell
RT mRNAs.";
RL Coll. Relat. Res. 6:239-248 (1986).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17823; AAB88016.1; -.
CC EMBL; M17820; AAB88016.1; JOINED.
CC EMBL; M17821; AAB88016.1; JOINED.
CC EMBL; M17822; AAB88016.1; JOINED.
CC EMBL; M19240; AAB88016.1; JOINED.
CC EMBL; M25663; AAB31203.1; -.
CC
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DR PIR; A27500; KCRBI.
DR HSSP; P03956; ICGL.
DR MEROPS; M10_001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001819; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MAIRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 18
FT PROPEP 19 98 Activation peptide.
FT CHAIN 99 468 Interstitial collagenase.
FT DOMAIN 274 468 Hemopexin-like.
FT SITE 91 91 Cysteine switch (Potential).
FT METAL 123 123 Calcium 1 (By similarity).
FT METAL 157 157 Calcium 2 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Zinc 1 (By similarity).
FT METAL 174 174 Calcium 3 (By similarity).
FT METAL 175 175 Calcium 3 (via carbonyl oxygen) (By
FT METAL 177 177 similarity).
FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
FT METAL 179 179 similarity).
FT METAL 182 182 Calcium 3 (via carbonyl oxygen) (By
FT METAL 189 189 similarity).
FT METAL 191 191 Zinc 1 (By similarity).
FT METAL 193 193 Calcium 2 (via carbonyl oxygen) (By
FT METAL 195 195 similarity).
FT METAL 197 197 Calcium 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 200 200 Calcium 3 (By similarity).
FT METAL 217 217 Calcium 3 (By similarity).
FT ACT_SITE 218 217 Zinc 2 (catalytic) (By similarity).
FT METAL 221 221 By similarity.
FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
FT METAL 284 284 Zinc 2 (catalytic) (By similarity).
FT METAL 328 328 Calcium 4 (via carbonyl oxygen) (By
FT METAL 377 377 similarity).
FT METAL 426 426 Calcium 4 (via carbonyl oxygen) (By
FT CARBOHYD 119 119 similarity).
FT DISULFID 277 465 N-linked (GlcNAc...) (Probable).
FT SEQUENCE 468 AA; 53739 MW; DA90538919952B8C CRC64;

Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 4.3e-20;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTFCNPKWERTNLTIRNY 55
    |||||
Db 66 MQRFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTFCNPKWERTNLTIRNY 120

RESULT 3
MM01_PIG
```

ID	MW01_PIG	STANDARD;	PRT;	469 AA.	
AC	P21692;				DR InterPro; IPR001818; Pept M10A_M12B.
DT	01-WAY-1991 (Rel. 18, Created)				DR InterPro; IPR006025; Pept M_Zn_BS.
DT	01-DEC-1992 (Rel. 24, Last sequence update)				DR InterPro; IPR009070; PGBD-like
DT	01-OCT-2004 (Rel. 45, Last annotation update)				DR Pfam; PF00045; Hemopexin_4.
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).				DR Pfam; PF00413; Peptidase M10; 1.
GN	Name=MMP1;				DR PRINTS; PR00138; MATRININ.
OS	Sus scrofa (Pig).				DR SMART; SM00120; HX; 4.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DR PROSITE; PS00235; ZmC; 1.
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
OX	NCBI_TaxID=9823;				DR PROSITE; PS00024; HEMOPEXIN; 1.
RN	[1]	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			DR PROSITE; PS00142; ZINC PROTEASE; 1.
RP	MEDLINE=91333421; PubMed=1651440;				KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
RA	Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;				KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
RT	"Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of expression of RNA in vitro by various cytokines.";				KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
RL	Matrix 11:161-167(1991).				KW Zymogen.
RN	[2]	SEQUENCE OF 25-469 FROM N.A.			FT SIGNAL 1 19
RP	TISSUE=Synovial cell;				FT PROPEP 20 99
RC	MEDLINE=91067477; PubMed=2174547;				FT CHAIN 100 469
RA	Clarke N.J., O'Hare M.C., Gawston T.E., Harper G.P.;				FT CHAIN 100 258
RT	"Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.";				FT DOMAIN 275 469
RL	Nucleic Acids Res. 18:6703-6703(1990).				FT SITE 92 92
RN	[3]				FT SITE 258 259
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.				FT METAL 124 124
RC	MEDLINE=96173003; PubMed=8590015;				FT METAL 158 158
RA	Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,				FT METAL 168 168
RA	Clark I.M., Bigg H.F., Hazleman B.L., Gawston T.E., Blow D.M.;				FT METAL 170 170
RT	"Structure of full-length porcine synovial collagenase reveals a C-terminal domain containing a calcium-linked, four-bladed beta-propeller.";				FT METAL 175 175
RL	Structure 3:541-549(1995).				FT METAL 176 176
RN	[4]				FT METAL 178 178
RP	SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.				FT METAL 180 180
RC	MEDLINE=95142615; PubMed=7840605;				FT METAL 183 183
RA	Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Gawston T.E.,				FT METAL 190 190
RA	O'Hare M.C.;				FT METAL 192 192
RT	"Recombinant porcine collagenase: purification and autolysis.";				FT METAL 196 196
RL	Arch. Biochem. Biophys. 316:123-127(1995).				FT METAL 198 198
CC	-!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X.				FT METAL 199 199
CC	-!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly- -Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.				FT METAL 201 201
CC	-!- COPACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.				FT METAL 218 218
CC	-!- ENZYME REGULATION: Can be activated without removal of the activation peptide.				FT ACT_SITE 219 219
CC	-!- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment having reduced catalytic activity.				FT METAL 222 222
CC	-!- SIMILARITY: Belongs to peptidase family M10A.				FT METAL 228 228
CC	-!- SIMILARITY: Contains 1 hemopexin-like domain.				FT METAL 285 285
CC	-----				FT METAL 329 329
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				FT METAL 378 378
CC	-----				FT METAL 427 427
CC	EMBL; X54724; CAA38526.1; -.				FT DISULFID 278 466
DR	PIR; S15986; KCPGI.				FT CARBOHYD 120 120
DR	PDB; 1FBL; X-ray; @=100-469.				FT STRAND 101 102
DR	MEROPS; M10.001; -.				FT STRAND 104 105
DR	InterPro; IPR000585; Hemopexin.				FT TURN 104 105
DR	InterPro; IPR006026; Peptidase_M.				FT STRAND 113 118
					FT TURN 123 124
					FT TURN 127 142
					FT HELIX 127 142
					FT TURN 143 144
					FT STRAND 148 152
					FT STRAND 159 164
					FT STRAND 182 184
					FT TURN 190 193
					FT STRAND 195 198
					FT TURN 199 200
					FT STRAND 204 204
					FT STRAND 211 211
					FT HELIX 212 223
					FT TURN 224 225
					FT STRAND 226 227
					FT TURN 232 233
					FT TURN 235 236
					FT HELIX 250 260
					FT TURN 277 278
					FT TURN 280 281
					FT STRAND 286 290
					FT TURN 291 292

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FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT HELIX 364 368
FT TURN 372 373
FT STRAND 379 383
FT TURN 384 387
FT STRAND 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 7.6e-20;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MOREFLGNTGKPNETLDMKKPCGVPDSCGFMLTGCPKWTNTLTIRNY 55
DB 67 MQQFGLKVGTPDPAETLNVKQPCGVPDVAEFLTPGNPWNTHLTIRNY 121

RESULT 4
MM08 RAT STANDARD; PRT; 466 AA.
AC O88766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowe D., Wells G., Burel S., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of
RT rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
CC type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By
```

DOMAIN	275	469	Homoeplexin-like.
T SITE	92	92	Cysteine switch.
T METAL	124	124	Calcium 1 (By similarity).
T METAL	158	158	Calcium 2 (By similarity).
T METAL	168	168	Zinc 1 (By similarity).
T METAL	170	170	Zinc 1 (By similarity).
T METAL	175	175	Calcium 3 (By similarity).
T METAL	176	176	Calcium 3 (via carbonyl oxygen) (By similarity).
T METAL	178	178	Calcium 3 (via carbonyl oxygen) (By similarity).
T METAL	180	180	Calcium 3 (via carbonyl oxygen) (By similarity).
T METAL	183	183	Zinc 1 (By similarity).
T METAL	190	190	Calcium 2 (via carbonyl oxygen) (By similarity).
T METAL	192	192	Calcium 2 (via carbonyl oxygen) (By similarity).
T METAL	194	194	Calcium 2 (By similarity).
T METAL	196	196	Zinc 1 (By similarity).
T METAL	198	198	Calcium 3 (By similarity).
T METAL	199	199	Calcium 3 (By similarity).
T METAL	201	201	Calcium 3 (By similarity).
T METAL	218	218	Zinc 2 (catalytic) (By similarity).
T ACT SITE	219	219	By similarity.
T METAL	222	222	Zinc 2 (catalytic) (By similarity).
T METAL	228	228	Zinc 2 (catalytic) (By similarity).
T METAL	285	285	Calcium 4 (via carbonyl oxygen) (By similarity).
T METAL	329	329	Calcium 4 (via carbonyl oxygen) (By similarity).
T METAL	378	378	Calcium 4 (via carbonyl oxygen) (By similarity).
T METAL	427	427	Calcium 4 (via carbonyl oxygen) (By similarity).
T DISULFID	278	466	By similarity.
T SEQUENCE	469 AA; 54001 MW; AEE6760AB2C529CA CRC64;		

Query Match 72.3%; Score 222; DB 1; Length 469;  
Best Local Similarity 70.9%; Pred. No. 9.8e-19;  
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 55

1 MOREFGLVTKGNETLDMKKPRCGVDPDGGGFMLEPGNPKWERTNLTIRNY 55  
67 MQEFGKLVTKGPDATLNVWKPQRCGVDPDAEFLVTEGNRWENTHLYRIENY 121

RESULT 6  
MM001: HUMAN  
D MM001 HUMAN STANDARD; PRT; 469 AA.  
C P3956; P08156;  
T 23-OCT-1986 (Rel. 02, Created)  
T 01-DEC-1992 (Rel. 24, Last sequence update)  
T 01-OCT-2004 (Rel. 45, Last annotation update)  
E Interstitial collagenase precursor (EC 3.4.24.7) (Matrix  
E metalloproteinase-1) [MMP-1] (Fibroblast collagenase).  
N Name=MMP1; Synonyms=CLG;  
N Homo sapiens (Human).  
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
S Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
X NCBI\_TaxID=9606;  
X [1] \_SEQUENCE FROM N.A.  
P MEDLINE=90352587; PubMed=2167156;  
X Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.  
X Stefler-Stevenson W.G.;  
X "Cloning and characterization of human tumor cell interstitial  
X collagenase.";  
X Cancer Res. 50:5431-5437(1990).  
X [2]  
P SEQUENCE FROM N.A.  
X MEDLINE=87156645; PubMed=3030290;  
X Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.

RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
RT "Comparison of human stromelysin and collagenase by cloning and  
RL sequence analysis.",  
RN Biochem. J. 240:913-916(1986).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=86196089; PubMed=3009463;  
RX Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,  
RA Eisen A.Z.;  
RA "Human fibroblast collagenase. Complete primary structure and homology  
RT to an oncogene transformation-induced rat protein.",  
RL J. Biol. Chem. 261:6600-6605(1986).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
RA Heller R., Davis R.W.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
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RP TISSUE=Ovary;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RN SEQUENCE OF 1-35 FROM N.A.  
RX MEDLINE=87257941; PubMed=3037355;  
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,  
RA Herrlich P.;  
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human  
RT collagenase gene is mediated by an inducible enhancer element located  
RT in the 5'-flanking region.",  
RL Mol. Cell. Biol. 7:2256-2266(1987).  
RN [7]  
RN SEQUENCE OF 1-70 FROM N.A.  
RC TISSUE=Synovial cell;  
RX MEDLINE=87109799; PubMed=3027129;  
RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;  
RT "Molecular cloning of human synovial cell collagenase and selection of  
RT a single gene from genomic DNA.",  
RL J. Clin. Invest. 79:542-546(1987).  
RN [8]  
RN SEQUENCE OF 100-112 AND 270-287.  
RC TISSUE=Fibroblast;  
RX MEDLINE=90104231; PubMed=2557822;  
RA Clark I.M., Cawston T.E.;  
RT "Fragments of human fibroblast collagenase. Purification and  
RT characterization.",  
RL Biochem. J. 263:201-206(1989).  
RN [9]  
RN SIMILARITY TO THERMOLYSIN TYPE PROTEASES.  
RX MEDLINE=87194799; PubMed=3032950;  
RA McKerrow J.H.;  
RT "Human fibroblast collagenase contains an amino acid sequence  
homologous to the zinc-binding site of Serratia protease.",  
RL J. Biol. Chem. 262:5943-5943(1987).  
RN [10]  
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.  
RX MEDLINE=95384760; PubMed=7656013;  
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,  
RA Brown P.A., Johnson W.H., Murray E.J.;  
RT "Structure of the catalytic domain of human fibroblast collagenase  
RT complexed with an inhibitor.",  
RL Nat. Struct. Biol. 1:106-110(1994).  
RN [11]  
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.  
RX MEDLINE=94304829; PubMed=8031754;  
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;  
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase  
RT complexed to itself.",  
RL Biochemistry 33:8207-8217(1994).  
RN [12]  
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.  
RX MEDLINE=94105765; PubMed=8278810;  
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,  
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,  
RA Jordan S.R.;  
RT "Structure of the catalytic domain of fibroblast collagenase complexed  
RT with an inhibitor.",  
RL Science 263:375-377(1994).  
RN [13]  
RN X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.  
RX MEDLINE=94377426; PubMed=8090713;  
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,  
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;  
RT "1.56-A structure of mature truncated human fibroblast collagenase.",  
RL Proteins 19:98-109(1994).  
RN [14]  
RN STRUCTURE BY NMR OF 101-269.  
RX MEDLINE=98145213; PubMed=9484219;  
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,  
RA Powers R.;  
RT "High-resolution solution structure of the inhibitor-free catalytic  
RT fragment of human fibroblast collagenase determined by  
RT multidimensional NMR.",  
RL Biochemistry 37:1495-1504(1998).  
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in  
CC the helical domain. Also cleaves collagens of types VII and X.  
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
CC collagen. Cleavage of the triple helix of collagen at about three-  
CC quarters of the length of the molecule from the N-terminus, at  
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
CC substrates and alpha-macroglobulins at bonds where p1' is a  
CC hydrophobic residue.  
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
CC -!- ENZYME REGULATION: Can be activated without removal of the  
CC activation peptide.  
CC -!- DOMAIN: There are two distinct domains in this protein; the  
CC catalytic N-terminal, and the C-terminal which is involved in  
CC substrate specificity and in binding TIMP (tissue inhibitor of  
CC metalloproteinases).  
CC -!- PTM: Undergoes autocatalytic cleavage to two major forms (22 kDa and  
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22  
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form  
CC can act as activator for collagenase.  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X05233; CAA28858.1; -.

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DR EMBL; M13509; AAA35699.1; -
DR EMBL; M16567; AAA52033.1; -
DR EMBL; U78045; AAB36941.1; -
DR EMBL; BC013875; AAH13875.1; -
DR EMBL; M15996; AAA35700.1; -
DR EMBL; X54925; CAA38691.1; -
DR PIR; A37308; KCHUI.
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGF; X-ray; @=102-269.
DR PDB; 1CGE; X-ray; A/B=102-269.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -
DR GlycosuiteDB; P03956; -
DR Genew; HGNC:7155; MMP1.
DR MIM; 120353; -; F.collagenase activity; TAS.
DR GO; GO:0008133; F.zinc ion binding; TAS.
DR GO; GO:0008270; P.proteolysis and peptidolysis; TAS.
DR GO; GO:0006508; P.proteolysis and peptidolysis; TAS.
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DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.

Query Match 72.0%; Score 221; DB 1; Length 469;
Best Local Similarity 70.9%; Pred.No. 1.3e-18;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMKKPRCGVDPDGGFVMTLPGNPKWERTNLTIRNY 55
DB 67 MQEFFGLKVTGKPDATLTKVMKQRCGVDPDVAQFVLTEGNPRWEQHLTYRIENY 121

RESULT 7
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AC AAP35520;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DE Matrix metalloproteinase 1 (interstitial collagenase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kainane N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RW EMBL; BT006874; AAP35520.1; -
KW Collagen.
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Query Match 72.0%; Score 221; DB 2; Length 469;
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Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKNEETLDMKKPRCGVDPDGGFVMTLPGNPKWERTNLTIRNY 55
DB 67 MQEFFGLKVTGKPDATLTKVMKQRCGVDPDVAQFVLTEGNPRWEQHLTYRIENY 121

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RESULT 8
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ID MM01_BOVIN
AC P28053;
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DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Bovinae; Bos.
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RC TISSUE=Periodontium fibroblast;
RC MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence."
RL DNA Seq. 5:61-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=1311165;
RX Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D.,
RA Parks W.C.;
RT "Purification and characterization of bovine interstitial collagenase
RT and tissue inhibitor of metalloproteinases."
RL Arch. Biochem. Biophys. 293:370-376(1992).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-1-le-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58256; CAA41210.1; -
CC PIR; S14554; KCBO1.
CC HSPF; P03956; LHFC.
CC MEROPS; M10.001; -
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase_M.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR009070; PGSD_like.
CC Pfam; PF00045; Hemopexin; 4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00138; MATRININ.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Direct protein sequencing;
KW

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FT METAL 169 Calcium 3 (By similarity).  
FT METAL 170 Calcium 1 (By similarity).  
FT METAL 172 Calcium 3 (By similarity).  
FT METAL 189 Zinc 2 (catalytic) (By similarity).  
FT ACT SITE 190 By similarity.  
FT METAL 193 Zinc 2 (catalytic) (By similarity).  
FT METAL 199 Zinc 2 (catalytic) (By similarity).  
FT METAL 249 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT METAL 277 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT METAL 347 Calcium 4 (via carbonyl oxygen) (By similarity).  
FT DISULFID 242 381 By similarity.  
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Db 57 LKQFFGLKVTGKPDATL-VMKQSTCGVPDVGVEYVLTFCNPRWENTHLYTRIENY 110  
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DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F73004H20 product:matrix  
DE Metalloprotease 8, full insert sequence.  
DE Name=Mmp8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
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RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M., Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
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RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
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RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Carninci P., Hayashizaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;  
RX MEDLINE=20530913; PubMed=11076961;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK089516; BAC40911.1; -;  
DR HSP; P22894; IJAP.  
DR MGD; MGI:11202395; Mmp8.  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M10A\_M12B.  
DR InterPro; IPR009070; PGBD-like.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase M10\_N; 1.  
DR PRINTS; PR00138; MATRINX.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZnMc; 1.  
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.  
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Db 66 MQRFFSLAETGKLDATMGIMPRCGVPDGGFLLTGPSPKWTHTNLTIRINH 120  
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DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F73001B13 product:matrix  
DE Metalloprotease 8, full insert sequence.  
GN Name=Mmp8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;



[1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=92279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX The FANTOM Consortium.  
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=2030913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Katsurai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK093381; BAC40862.1; -;  
 DR HSP; F22894; IJAP.  
 DR MGD; MGI:1203195; Mmp8.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept M10A M12B.  
 DR InterPro; IPR006025; Pept M Zn BS.  
 DR InterPro; IPR009070; PGSD-like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase\_M10; 1.

DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZmC; 1.  
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 465 AA; 53114 MW; F80522831AACB4E2 CRC64;  
 Query Match 64.5%; Score 198; DB 2; Length 465;  
 Best Local Similarity 65.5%; Pred. No. 9e-16;  
 Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTKPNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55  
 DQ 66 MQRFFSLAETGKLDAAATMGIMEMPRCGVPSGGFLLTPGSKWTHNLTIRINH 120  
 RESULT 12  
 AAH42742 PRELIMINARY; PRT; 465 AA.  
 AC AAH42742;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Matrix metalloproteinase 8.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;  
 RX MEDLINE=22389257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klatschner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyx S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC042742; AAH42742.1; -;  
 SQ SEQUENCE 465 AA; 53125 MW; 448AEC59639E9237 CRC64;

Query Match 64.5%; Score 198; DB 2; Length 465;  
 Best Local Similarity 65.5%; Pred. No. 9e-16;  
 Matches 36; Conservative 7; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MQRFFGLNVTKPNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55  
 DQ 66 MQRFFSLAETGKLDAAATMGIMEMPRCGVPSGGFLLTPGSKWTHNLTIRINH 120  
 RESULT 13  
 BAC40805



Query Match 64.5%; Score 198; DB 2; Length 478;  
Best Local Similarity 63.6%; Pred. No. 9.3e-16;  
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

1 MQRFFGLNVTKPNEETLDMKKPRGVPDGGFMLTPGNPKWERTNLTIRINY 55  
 67 MQKFLGLEVTGKVDSDTLAMRRRPRGVPDVGDFTTTFGMPKVRKTHLTIRINY 121

Search completed: October 13, 2004, 15:14:41  
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